

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:17:29 : Search time 3114 Seconds
(without alignments)
4093.526 Million cell updates/sec

Title: US-09-975-456B-1

Perfect score: 507

Sequence: 1 atgaagaagtcttcacagt.....cgccccccgcctccctccag 507

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/US06_PCTUS_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq.*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq.*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq.*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq.*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq.*
16: /cgn2_6/ptodata/2/pna/US092_COMB.seq.*
17: /cgn2_6/ptodata/2/pna/US093_COMB.seq.*
18: /cgn2_6/ptodata/2/pna/US094_COMB.seq.*
19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq.*
20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq.*
21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq.*
22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
23: /cgn2_6/ptodata/2/pna/US095E_COMB.seq.*
24: /cgn2_6/ptodata/2/pna/US095F_COMB.seq.*
25: /cgn2_6/ptodata/2/pna/US095G_COMB.seq.*
26: /cgn2_6/ptodata/2/pna/US095H_COMB.seq.*
27: /cgn2_6/ptodata/2/pna/US095I_COMB.seq.*
28: /cgn2_6/ptodata/2/pna/US095J_COMB.seq.*
29: /cgn2_6/ptodata/2/pna/US095K_COMB.seq.*
30: /cgn2_6/ptodata/2/pna/US095L_COMB.seq.*
31: /cgn2_6/ptodata/2/pna/US095M_COMB.seq.*
32: /cgn2_6/ptodata/2/pna/US095N_COMB.seq.*
33: /cgn2_6/ptodata/2/pna/US095O_COMB.seq.*
34: /cgn2_6/ptodata/2/pna/US095P_COMB.seq.*
35: /cgn2_6/ptodata/2/pna/US095Q_COMB.seq.*
36: /cgn2_6/ptodata/2/pna/US095R_COMB.seq.*
37: /cgn2_6/ptodata/2/pna/US095S_COMB.seq.*
38: /cgn2_6/ptodata/2/pna/US095T_COMB.seq.*
39: /cgn2_6/ptodata/2/pna/US095U_COMB.seq.*
40: /cgn2_6/ptodata/2/pna/US095V_COMB.seq.*
41: /cgn2_6/ptodata/2/pna/US095W_COMB.seq.*
42: /cgn2_6/ptodata/2/pna/US095X_COMB.seq.*
43: /cgn2_6/ptodata/2/pna/US095Y_COMB.seq.*

44: /cgn2_6/ptodata/2/pna/US6000_COMB.seq.*
45: /cgn2_6/ptodata/2/pna/US6001_COMB.seq.*
46: /cgn2_6/ptodata/2/pna/US6002_COMB.seq.*
47: /cgn2_6/ptodata/2/pna/US6003_COMB.seq.*
48: /cgn2_6/ptodata/2/pna/US6004_COMB.seq.*
49: /cgn2_6/ptodata/2/pna/US6005_COMB.seq.*
50: /cgn2_6/ptodata/2/pna/US6006_COMB.seq.*
51: /cgn2_6/ptodata/2/pna/US6007_COMB.seq.*
52: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
53: /cgn2_6/ptodata/2/pna/US6009_COMB.seq.*
54: /cgn2_6/ptodata/2/pna/US6010_COMB.seq.*
55: /cgn2_6/ptodata/2/pna/US6011_COMB.seq.*
56: /cgn2_6/ptodata/2/pna/US6012_COMB.seq.*
57: /cgn2_6/ptodata/2/pna/US6013_COMB.seq.*
58: /cgn2_6/ptodata/2/pna/US6014_COMB.seq.*
59: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
60: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
61: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
62: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
63: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
64: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
65: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
66: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
67: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
68: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
69: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
70: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
71: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
72: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
73: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
74: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
75: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
76: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
77: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
78: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
79: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
80: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*
81: /cgn2_6/ptodata/2/pna/US6037_COMB.seq.*
82: /cgn2_6/ptodata/2/pna/US6038_COMB.seq.*
83: /cgn2_6/ptodata/2/pna/US6039_COMB.seq.*
84: /cgn2_6/ptodata/2/pna/US6040_COMB.seq.*
85: /cgn2_6/ptodata/2/pna/US6041_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	507	100.0	507	US-09-975-456B-1	Sequence 1, Appl
2	507	100.0	2270	US-60-203-511-4	Sequence 4, Appl
3	507	100.0	2270	US-60-403-468-3	Sequence 3, Appl
4	505.4	99.7	2716	US-10-104-047-1765	Sequence 1765, Ap
5	464	91.5	748	US-60-212-356-317	Sequence 317, App
6	464	91.5	829	US-60-212-356-282	Sequence 282, App
7	379	74.8	379	US-60-229-525-741	Sequence 741, App
8	342.2	67.5	903	US-60-360-207-10397	Sequence 10397, A
9	305	60.2	748	US-60-229-525-724	Sequence 724, App
10	252.4	49.8	748	US-60-229-525-571	Sequence 571, App
11	240	47.3	256	US-60-234-446-1225	Sequence 1225, Ap
12	222.8	43.9	483	US-60-126-590-447	Sequence 447, App
13	212	41.8	627	US-60-160-203-829	Sequence 829, App
14	212	41.8	4179	US-60-207-316-43	Sequence 43, Appl
15	199.4	39.3	1644	US-09-609-137-56	Sequence 56, Appl
16	199.4	39.3	1644	US-10-137-659-56	Sequence 56, Appl
17	167.2	33.0	388	US-10-137-659-38	Sequence 38, Appl
18	167.2	33.0	388	US-10-137-659-38	Sequence 103, App
19	126	24.9	549	US-60-196-174-103	Sequence 686, App
20	115	22.7	712	US-60-177-571-686	Sequence 15647, A
21	110.8	21.9	560	US-09-634-306B-15647	Sequence 15647, A

C	22	110.8	21.9	560	38	US-10-027-632-15647	Sequence 15647, A
	23	100.6	19.8	549	17	US-09-362-510-22948	Sequence 22948, A
	24	100.6	19.8	549	17	US-09-362-510-22948	Sequence 22948, A
	25	100.6	19.8	549	18	US-09-489-036-8343	Sequence 8343, Ap
	26	100.6	19.8	549	34	US-09-904-013-22948	Sequence 22948, A
	27	100.6	19.8	549	35	US-09-943-143-8343	Sequence 8343, Ap
	28	99.4	19.6	674	19	US-09-528-409-31852	Sequence 31852, A
	29	99.4	19.6	674	35	US-09-933-524-31852	Sequence 31852, A
	30	99.4	19.6	674	35	US-09-933-524-31852	Sequence 31852, A
	31	99	19.5	451	19	US-09-528-409-70519	Sequence 70519, A
	32	99	19.5	451	35	US-09-933-524-70519	Sequence 70519, A
	33	99	19.5	451	35	US-09-933-524-70519	Sequence 70519, A
	34	99	19.5	476	18	US-09-489-036-30282	Sequence 30282, A
	35	99	19.5	476	35	US-09-943-143-30282	Sequence 30282, A
	36	99	19.5	592	15	US-09-181-317-3	Sequence 3, Appli
	37	99	19.5	719	19	US-09-528-409-68551	Sequence 68551, A
	38	99	19.5	719	35	US-09-933-524-68551	Sequence 68551, A
	39	99	19.5	719	35	US-09-933-524-68551	Sequence 68551, A
	40	99	19.5	854	1	PCT-US01-10542-6	Sequence 6, Appli
	41	99	19.5	854	36	US-09-369-384-6	Sequence 6, Appli
	42	99	19.5	878	32	US-09-856-486-26	Sequence 26, Appli
	43	99	19.5	901	65	US-60-212-356-281	Sequence 281, App
	44	99	19.5	1687	17	US-09-347-127-91	Sequence 91, Appl
	45	99	19.5	1687	34	US-09-905-059-91	Sequence 91, Appl

ALIGNMENTS

```

RESULT 1
US-09-975-456B-1
? Sequence 1: Application US/09975456B
? GENERAL INFORMATION:
? APPLICANT: LAZDUNSKI, MICHEL
? APPLICANT: LAMBEAU, GERARD
? APPLICANT: VALENTIN, EMMANUEL
? TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
? FILE REFERENCE: 1478-R-00
? CURRENT APPLICATION NUMBER: US/09/975,456B
? CURRENT FILING DATE: 2002-08-27
? PRIOR APPLICATION NUMBER: 60/239,491
? PRIOR FILING DATE: 2000-10-11
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: PatentIn version 2.1
? SEQ ID NO 1
? LENGTH: 507
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(507)
? OTHER INFORMATION: cDNA encoding human group IIF
US-09-975-456B-1

```

Query Match	100.0%	Score 507;	DB 36;	Length 507;
Best Local Similarity	100.0%;	Pred. No. 1.1e-115;		
Matches 507;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAGAAGTTCTTACCGTGGCCATCCTTCTGGCAGCGTTCTGTCCACAGCTCACGGC	60	
Db	1	ATGAAGAAGTTCTTACCGTGGCCATCCTTCTGGCAGCGTTCTGTCCACAGCTCACGGC	60	
QY	61	AGCCTGTCTCAACTGGAAGGCCATGTGTGAGGCGCTCACAGGAGGAGCGCCATCCTGTCC	120	
Db	61	AGCCTGTCTCAACTGGAAGGCCATGTGTGAGGCGCTCACAGGAGGAGCGCCATCCTGTCC	120	
QY	121	TTCTGTGGGCTACGGTTGCTTACTGTGGGCTGGGGGCGCTGGCCAGCCCAAGGATGAGGTG	180	
Db	121	TTCTGTGGGCTACGGTTGCTTACTGTGGGCTGGGGGCGCTGGCCAGCCCAAGGATGAGGTG	180	
Y	181	GACTGTGTCTGCCAGCCACGACTGCTGTACAGAACTCTTTGACCAAGGCTGTCAAC	240	
b	181	GACTGTGTCTGCCAGCCACGACTGCTGTACAGAACTCTTTGACCAAGGCTGTCAAC	240	

QY	241	CCCTATGTGGACCACTATGATCACACCATCGAGAACAACTGAGATAGTCTGCAGTGAC	300
Db	241	CCCTATGTGGACCACTATGATCACACCATCGAGAACAACTGAGATAGTCTGCAGTGAC	300
QY	301	CTCAACAAGACAGAGTGTGACAACGACAGATGCTGTGACAAGAACATGGTCTGTGC	360
Db	301	CTCAACAAGACAGAGTGTGACAACGACAGATGCTGTGACAAGAACATGGTCTGTGC	360
QY	361	CTCATGACCAACGAGTACCGAGAGGAGTACCGTGGCTTCCCTCAATGCTACTGCCAGGGC	420
Db	361	CTCATGACCAACGAGTACCGAGAGGAGTACCGTGGCTTCCCTCAATGCTACTGCCAGGGC	420
QY	421	CCACGCCCAACTGCAGCATCTATGAACGCCGCCCTGAGGAGGTCACTGCAGTCACCAA	480
Db	421	CCACGCCCAACTGCAGCATCTATGAACGCCGCCCTGAGGAGGTCACTGCAGTCACCAA	480
QY	481	TCCCGAGCGCCCCCGCCCTCCCTAG	507
Db	481	TCCCGAGCGCCCCCGCCCTCCCTAG	507

RESULT 2

```

US-60-203-511-4
; Sequence 4, Application US/60203511
; GENERAL INFORMATION:
; APPLICANT: Das, Debopriya
; APPLICANT: Reddy, Roopa
; APPLICANT: Yao, Monique G.
; APPLICANT: Nguyen, Danniel B.
; APPLICANT: Lu, Yan
; APPLICANT: Tribouley, Catherine M.
; APPLICANT: Yue, Henry
; APPLICANT: Khan, Farrah A.
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0095 P
; CURRENT APPLICATION NUMBER: US/60/203,511
; CURRENT FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7473224CH1
US-60-203-511-4

```

[illegible]

; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317
; LENGTH: 748
; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-356-317

Query Match 91.5%; Score 464; DB 65; Length 748;
Best Local Similarity 100.0%; Pred. No. 5.9e-105;
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGAAGTCTTCCACCGTGGCCATCTTGTGTCAGCGTTCCTGTCACAGCTCAGCGC 60
DB 131 ATGAAGAAGTCTTCCACCGTGGCCATCTTGTGTCAGCGTTCCTGTCACAGCTCAGCGC 190
QY 61 AGCCTGCTCAACCTGAAGGCCATGTGGAGGCCGTCACAGGAGGAGGCGCATCCTGTGC 120
DB 191 AGCCTGCTCAACCTGAAGGCCATGTGGAGGCCGTCACAGGAGGAGGCGCATCCTGTGC 250
QY 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTCAGGAGGAGGAGGAGGAGG 180
DB 251 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTCAGGAGGAGGAGGAGGAGG 310
QY 181 GACTGGTGTGCGCAGCGCCAGCTGCTGCTACCAAGAACTCTTTGACCAAGGCTGTCC 240
DB 311 GACTGGTGTGCGCAGCGCCAGCTGCTGCTACCAAGAACTCTTTGACCAAGGCTGTCC 370
QY 241 CCTATGTGGACACTATGATACACCATCGAGAACACACTGAGATAGTCTGCAGTGAC 300
DB 371 CCTATGTGGACACTATGATACACCATCGAGAACACACTGAGATAGTCTGCAGTGAC 430
QY 301 CTCACAAAGACAGAGTGTGACAGCAGACATGATGTGTGACAAAGAACTGTTCTGTGC 360
DB 431 CTCACAAAGACAGAGTGTGACAGCAGACATGATGTGTGACAAAGAACTGTTCTGTGC 490
QY 361 CTCATGAACACAGAGTACCAGAGGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGCG 420
DB 491 CTCATGAACACAGAGTACCAGAGGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGCG 550
QY 421 CCCAGCGCCAACTGACGATCTATGAACCGCCCTGAGGAGGT 464
DB 551 CCCAGCGCCAACTGACGATCTATGAACCGCCCTGAGGAGGT 594

RESULT 6

US-60-212-356-282
; Sequence 282, Application US/60212356
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CL000677
; CURRENT APPLICATION NUMBER: US/60/212,356
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 829
; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-356-282

Query Match 91.5%; Score 464; DB 65; Length 829;
Best Local Similarity 100.0%; Pred. No. 5.9e-105;
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGAAGTCTTCCACCGTGGCCATCTTGTGTCAGCGTTCCTGTCACAGCTCAGCGC 60
DB 131 ATGAAGAAGTCTTCCACCGTGGCCATCTTGTGTCAGCGTTCCTGTCACAGCTCAGCGC 190

QY 61 AGCCTGCTCAACCTGAAGGCCATGTGGAGCGCTCACAGGAGGAGGCGCCATCTCTGTCC 120
DB 191 AGCCTGCTCAACCTGAAGGCCATGTGGAGCGCTCACAGGAGGAGGCGCCATCTCTGTCC 250
QY 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTCAGGAGGAGGAGGAGGAGG 180
DB 251 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTCAGGAGGAGGAGGAGGAGG 310
QY 181 GACTGGTGTGCGCAGCGCCAGCTGCTGCTACCAAGAACTCTTTGACCAAGGCTGTCC 240
DB 311 GACTGGTGTGCGCAGCGCCAGCTGCTGCTACCAAGAACTCTTTGACCAAGGCTGTCC 370
QY 241 CCTATGTGGACACTATGATACACCATCGAGAACACACTGAGATAGTCTGCAGTGAC 300
DB 371 CCTATGTGGACACTATGATACACCATCGAGAACACACTGAGATAGTCTGCAGTGAC 430
QY 301 CTCACAAAGACAGAGTGTGACAGCAGACATGATGTGTGACAAAGAACTGTTCTGTGC 360
DB 431 CTCACAAAGACAGAGTGTGACAGCAGACATGATGTGTGACAAAGAACTGTTCTGTGC 490
QY 361 CTCATGAACACAGAGTACCAGAGGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGCG 420
DB 491 CTCATGAACACAGAGTACCAGAGGAGTACCGTGGCTTCTCAATGTCTACTGCCAGGCG 550
QY 421 CCCAGCGCCAACTGACGATCTATGAACCGCCCTGAGGAGGT 464
DB 551 CCCAGCGCCAACTGACGATCTATGAACCGCCCTGAGGAGGT 594

RESULT 7

US-60-229-525-741
; Sequence 741, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 741
; LENGTH: 379
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-525-741

Query Match 74.8%; Score 379; DB 66; Length 379;
Best Local Similarity 100.0%; Pred. No. 7.1e-84;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 CGGACGCTGCTCAACCTGAAGGCCATGTGGAGCGCTCACAGGAGGAGGCGCCATCCT 116
DB 1 CGGACGCTGCTCAACCTGAAGGCCATGTGGAGCGCTCACAGGAGGAGGCGCCATCCT 60
QY 117 CTCCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTCAGGAGGAGGAGGAGG 176
DB 61 CTCCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGTCAGGAGGAGGAGGAGG 120
QY 177 GGTGGACTGTGTCGCCACGCCACGACTGCTGTACCAAGAACTCTTTGACCAAGGCTG 236
DB 121 GGTGGACTGTGTCGCCACGCCACGACTGCTGTACCAAGAACTCTTTGACCAAGGCTG 180
QY 237 TCACCCCTATGTGGACCACTATGATACACCATCGAGAACAACTGATAGTCTGCAG 296
DB 181 TCACCCCTATGTGGACCACTATGATACACCATCGAGAACAACTGATAGTCTGCAG 240
QY 297 TGACCTCAACAGACAGAGTGTGACAGCAGACATGATGTGTGACAAAGAACTGTTCT 356
DB 241 TGACCTCAACAGACAGAGTGTGACAGCAGACATGATGTGTGACAAAGAACTGTTCT 300
QY 357 GTGCTCATGAACACAGAGGTACCGAGGAGGAGTACCGTGGCTTCTCAATGTCTACTGCCA 416

|||||
Db 301 GTGCTCATGAACACAGAGTACCGAGAGGAGTACCGTGGCTTCTCAATGCTACTGCCA 360
QY 417 GGGCCCCACGCCCACTGC 435
Db 361 GGGCCCCACGCCCACTGC 379

RESULT 8

US-60-360-207-10397
; Sequence 10397, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 10397
; LENGTH: 903
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-10397

Query Match 67.5%; Score 342.2; DB 80; Length 903;
Best Local Similarity 79.7%; Pred. No. 1.2e-74;
Matches 404; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTCTTTCACCGTGGCCATCTTGCTGGCAGGCTTCTGTCCACAGCTCACGGC 60
Db 251 ATGAAGAATCTTTGCCATCGCAGTCTCGCGCGGAGTGTGGTAACACAGCCGCCACAGC 310
QY 61 AGCTGTCTCAACCTGAAGGCCATGTGTGGAGCGCTCACAGAGGAGGAGGCCCATCTGTGCC 120
-Db 311 AGCTGTCTGAACCTGAAGTCCATGTGTGGAGGCCATCACACAGAACTCCATCTGTGCC 370
QY 121 TTCTGGGCTACGGTCTACTGTGGCTGGGGGCGGCTGGCCAGGCCCAAGGATGAGGTG 180
Db 371 TTGTGGGCTACGGCTGCTACTCGGGCTGGGGGACGCGGCCATCCCCATGGATGAGGTA 430
QY 181 GACTGTGTGCCACGCCACGACTGCTGTACAGGAATCTTTGACCAAGGCTGTAC 240
Db 431 GACTGTGTGCCATGCCACGACTGTTGCTATGAGAAGCTTTTGAGCAGGCTTGGCCG 490
QY 241 CCTATGTGACCACTATGATACACCATCGAGAACACACTGAGATGCTGTGCACTGAC 300
Db 491 CCTATGTGACCACTATGACCAAGGATCGAGAATGGCACCATGATGTCTGTGCACTGAG 550
QY 301 CTCAACACAGACAGTGTGACAAGACAGATGCTGTGACAAGAACATGTTCTGTGTC 360
Db 551 CTCAATGACAGCGAGTGTGACAAGACAGATCGGAGTGTGACAAGAGCTGACTGTGTC 610
QY 361 CTCATGAACAGACAGTGTGACGAGGAGTACCGTGGCTTCTCAATGTCTACTGCGAGGGC 420
Db 611 CTCGAAGTACCCATACACAGGAACTACCGAGGCTACTTCAAGCTCTACTGCGAGGGC 670
QY 421 CCCACGCCCACTGACGATCTATGACCGCCCTGAGGAGGTACCTGCAAGTCAACAA 480
Db 671 CCCACACCACTGACGATCTATGACCGCTACCCAGAGGAATCACCTGTGGCATGGC 730
QY 481 TCCCCAGCCCCCGCCCTCCCTAG 507
Db 731 CTCCCTGGCAGCCCTCTCTCAACCTAG 757

RESULT 9

US-60-229-525-724
; Sequence 724, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; PROTEINS, AND USES THEREOF

; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 724
; LENGTH: 748
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-525-724

Query Match 60.2%; Score 305; DB 66; Length 748;
Best Local Similarity 83.2%; Pred. No. 2.1e-65;
Matches 347; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 91 GCCGTACAGGAGGAGCGGCATCTGCTCTGCTGGGCTACGGTTGCTACTGTGGGCTG 150
Db 171 GCCGTACAGGAGGAGCGGCATCTGCTCTGCTGGGCTACGGTTGCTACTGTGGGCTG 230
QY 151 GGGGGCGTGGCCAGCCCAAGGATGAGGTGAGTGTGCTGCCACGCCACGACTGCTGC 210
Db 231 GGGGGCGTGGCCAGCCCAAGGATGAGGTGAGTGTGAGTACACAGCGCTGGGCTCT 290
QY 211 TACCAGAACTCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCAATC 270
Db 291 GTCAGGGGCAAAATGAGGACAGCTGTGTCACCCCTATGTGGACCACTATGATCACCAATC 350
QY 271 GAGAACAACTGAGATAGTCTGACGTGACCTCAACAAGACAGAGTGTACAAAGCAGACA 330
Db 351 GAGAACAACTGAGATAGTCTGACGTGAGTCTGCTGCTCATGAACACAGACGTACCGAGGAGTAC 410
QY 331 TGCATGTGTGACAAGAACATGTTCTGTGCTCATGAACACAGACGTACCGAGGAGTAC 390
Db 411 AGGAGTGGTGGCTTAACATGTTCTGTGCTCATGAACACAGACGTACCGAGGAGTAC 470
QY 391 CGTGGCTTCTCAATGCTTACTGCCAGGGCCACGCCCACTGAGCATCTATCAACCG 450
Db 471 CGTGGCTTCTCAATGCTTACTGCCAGGGCCACGCCCACTGAGCATCTATGAACCG 530
QY 451 CCCCTGAGAGGTACCTGCTGACGTACCAATCCCCAGCCCCCCCCCTCCCTAG 507
Db 531 CCCCTGAGAGGTACCTGCTGACGTACCAATCCCCAGCCCCCCCCCTCCCTAG 587

RESULT 10

US-60-229-525-571
; Sequence 571, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 748
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-525-571

Query Match 49.8%; Score 252.4; DB 66; Length 748;
Best Local Similarity 77.9%; Pred. No. 2.6e-52;
Matches 304; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 40 GTTCTGTCCACAGCTACGCGAGCTGTCAACCTGAAGGCATGTGGAGGCGCTCACA 99
Db 220 GTTCTGTCCACAGCTACGCGAGCTGTCAACCTGAAGGCATGTGGAGGCGCTCACA 279
QY 100 GGGAGAGCGGCATCTCTCTTCTGTTGGGCTACCGTTGCTACTGTGGGCTGGGGCGCT 159
|||||

```

Db      280  G G A G G A G G C C C A T C T G T C C T T C G T G G C C T A C G G T A G A T G G C C C G G C C C A G C C A T G C C T   339
QY      160  G G C C A G C C C A A G G A T A G A G T G A C T G G T G C C A C C C C A C G A C T G C T G C T A C A G G A A   219
Db      340  G T C C A C T A C C T C T C C G C G T C C C T A G G T G C T G C C A C C C C A C G A C T G C T G C T A C C A G G A A   399
QY      220  C T C T T T G A C C A A G G T G T C A C C C C T A T G T G A C C A C T A T G A T C A C A C C A T C G A G A A C A C   279
Db      400  C T C T T T G A C C A A G G T G T C A C C C C T A G A G C T G T G C C C C T T C A T C C A G A G C C T T T G C C A   459
QY      280  A C T G A G A T A G T G C A G T G A C C T C A A C A G A G A G T G T G A C A A G C A G A C A T G C A T G T G T   339
Db      460  C C C A T C C C C C T G T A G G T G A C C T C A A C A G A C A G A G T G T G A C A A G C A G A C A T G C A T G T G T   519
QY      340  G A C A A G A A C A T G G T T C T G T G C C T C A T G A A C C A G A C G T A C C G A G A G A G T A C C G T G G C T T C   399
Db      520  G A C A A G A A C A T G G T T C T G T G C C T C A T G A C C A G A C A C T A C C G A G A G A G T A C C G T G G C T T C   579
QY      400  C T C A A T G T C T A C T G C C A G G G C C C A C G C C C   429
Db      580  C T C A A T G T C T A C T A A T A A A G G C C T C C T A C C   609

RESULT 11
US-60-234-446-1225
; Sequence 1225, Application US/60234446
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CLO00832
; CURRENT APPLICATION NUMBER: US/60/234,446
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 1797
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1225
.; LENGTH: 256
; TYPE: DNA
; ORGANISM: HUMAN
US-60-234-446-1225

Query Match      47.3%; Score 240; DB 67; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.6e-49;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      60  C A C C T G C T C A C C C T C A A G G C C A T G T G G A G G C C G T C A C A G G A G G A G G C C C A T C C T G T C   119
Db      1  C A C C T G C T C A C C C T G A A G G C C A T G T G A G G C C G T C A C A G G A G G A G G C C C A T C C T G T C   60
QY      120  C T T C T G G G C T A C G G T T G C T A C T G T G G C T G G G G G C C G T G C C A G C C C A A G A G A T G A G G T   179
Db      61  C T T C T G G G C T A C G T T T C T A C T G T G G C T G G G G G C C G T G C C A G C C C A A G A G A T G A G G T   120
QY      180  G G A C T G G T G C T C C C A G C C C A G A C T G C T G C T A C C A G G A A C T T T T G A C C A A G G C T G T C A   239
Db      121  G G A C T G G T G C T C C C A G C C C A G A C T G C T G C T A C C A G G A A C T T T T G A C C A A G G C T G T C A   180
QY      240  C C C T A T G T G G A C C A C T A T A T A C A C C A T C G A G A C A C A C T G A G A T A G T C T G C A G T G A   299
Db      181  C C C T A T G T G A C C A C T A T A T A C A C C A T C G A G A C A C A C T G A G A T A G T C T G C A G T G A   240

RESULT 12
US-60-126-590-447
; Sequence 447, Application US/60126590
; GENERAL INFORMATION:
; APPLICANT: Hodgson, David M.
; APPLICANT: Lincoln, Stephen E.
; APPLICANT: Russo, Frank D.
; APPLICANT: Spiro, Peter A.
; APPLICANT: Banville, Steve C.
; APPLICANT: Bratcher, Shawn R.

```

```
; SEQ ID NO 56
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-609-137-56

Query Match      39.3%; Score 199.4; DB 23; Length 1644;
Best Local Similarity 94.9%; Pred. No. 4.8e-39;
Matches 206; Conservative 0; Mismatches 11; Indels 0; Gaps

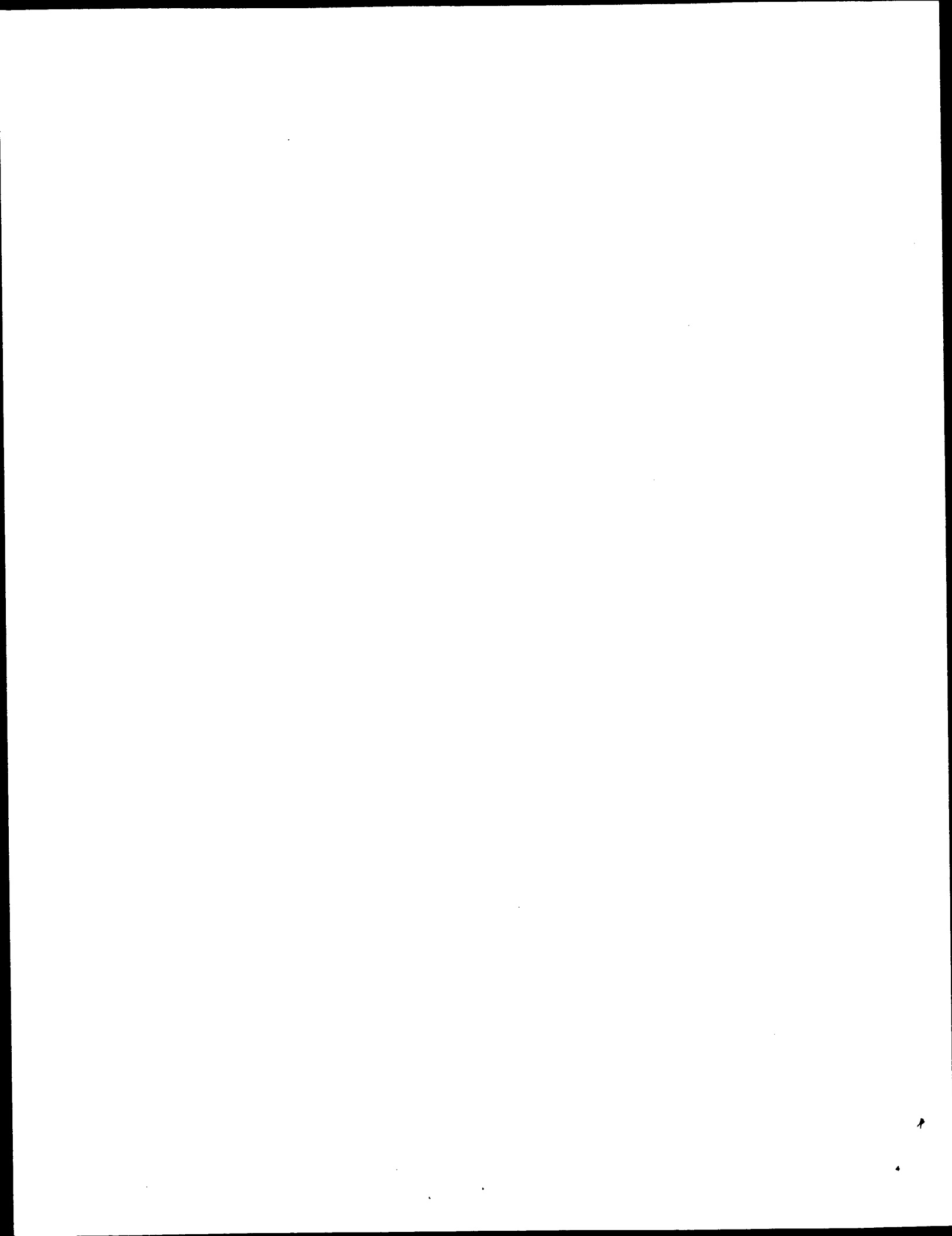
QY    291 CTGCAGTGCACCTCAACAAGACAGAGTGTCACAAGCAGACATGTCATGTGTGCACAGAACAT 350
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ddb   45 CTCAGGTGACCTCAACNAGCAGAGTGTCACRAAGCAGACATGCGATGTGTGACAAGAACAT 104

QY    351 GGTTCTGTGGCTCATGAACCAGACGTCACGAGAGGAGTACCGTGGCTTCCTCAATGTCTA 410
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ddb   105 GGTTCTGTGGCTCATGAACCAGAGGTACCGAGAGGAGTACCGTGGCTTCCTCAANTGTCTA 164

QY    411 CTGCCAGGGCCCCACGGCCAACTGCAGACATCTATGAACGCCGCCCTCAGGAGGTTCACCTG 470
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ddb   165 CTGCCAGGGCCCCACGCCAACTGCAGACATCTATGAACGCCGCCCTCAGGAGGTTCACCTG 224

QY    471 CAGTCCACAATCCCAGCGCCCCCCCCCTCCCTTAG 507
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ddb   225 CAATCAAATAATCACACCGCCCCCCCCCTCCCAACCCAG 261
```

Search completed: February 8, 2003, 06:38:30
Job time : 3119 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:36:59 : Search time 182 Seconds
(without alignments)
3602.321 Million cell updates/sec

Title: US-09-975-456B-1

Perfect score: 507

Sequence: 1 atgaagaagtcttcacgtg.....cgccccccgccccctccctag 507

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2558245 seqs, 646570469 residues

Total number of hits satisfying chosen parameters: 5116490

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	100.0	2270	6	US-10-275-998-7
2	507	100.0	2297	1	PCT-US02-21338-79
3	507	100.0	2297	6	US-10-188-832-79
4	99	19.5	1327	6	US-10-276-781-616
5	99	19.5	1938	5	US-09-949-002-110
6	99	19.5	1938	5	US-09-949-002-110
7	99	19.5	2747	1	PCT-US02-29560-195
8	99	19.5	2747	6	US-10-245-882-195
9	95.6	18.9	496	6	US-10-131-813A-533
10	95.6	18.9	496	6	US-10-131-819A-533
11	95.6	18.9	496	6	US-10-131-823A-533
12	95.6	18.9	496	6	US-10-131-824A-533
13	95.6	18.9	496	6	US-10-131-826A-533
14	95.6	18.9	496	6	US-10-131-829A-533
15	95.6	18.9	496	6	US-10-125-926A-533
16	95.6	18.9	496	6	US-10-127-829A-533
17	95.6	18.9	496	6	US-10-127-831A-533
18	95.6	18.9	496	6	US-10-127-835A-533
19	95.6	18.9	496	6	US-10-127-837A-533
20	95.6	18.9	496	6	US-10-127-842A-533
21	95.6	18.9	496	6	US-10-127-850A-533
22	95.6	18.9	496	6	US-10-127-901A-533
23	95.6	18.9	496	6	US-10-128-689A-533
24	95.6	18.9	496	6	US-10-131-830A-533
25	95.6	18.9	496	6	US-10-131-833A-533
26	95.6	18.9	496	6	US-10-131-837A-533

27	95.6	18.9	496	6	US-10-125-930A-533	Sequence 533, App
28	95.6	18.9	496	6	US-10-127-825A-533	Sequence 533, App
29	95.6	18.9	496	6	US-10-127-838B-533	Sequence 533, App
30	95.6	18.9	496	6	US-10-127-843A-533	Sequence 533, App
31	95.6	18.9	496	6	US-10-127-849A-533	Sequence 533, App
32	95.6	18.9	496	6	US-10-128-684A-533	Sequence 533, App
33	95.6	18.9	496	6	US-10-128-685A-533	Sequence 533, App
34	95.6	18.9	496	6	US-10-128-686A-533	Sequence 533, App
35	95.6	18.9	496	6	US-10-128-690A-533	Sequence 533, App
36	95.6	18.9	496	6	US-10-128-693A-533	Sequence 533, App
37	95.6	18.9	496	6	US-10-131-821A-533	Sequence 533, App
38	95.6	18.9	496	6	US-10-131-836A-533	Sequence 533, App
39	95.6	18.9	496	6	US-10-137-872A-533	Sequence 533, App
40	95.6	18.9	496	6	US-10-137-873A-533	Sequence 533, App
41	95.6	18.9	496	6	US-10-125-921A-533	Sequence 533, App
42	95.6	18.9	496	6	US-10-125-928A-533	Sequence 533, App
43	95.6	18.9	496	6	US-10-127-822A-533	Sequence 533, App
44	95.6	18.9	496	6	US-10-127-824A-533	Sequence 533, App
45	95.6	18.9	496	6	US-10-127-824A-533	Sequence 533, App

ALIGNMENTS

RESULT 1
US-10-275-998-7
: Sequence 7, Application US/10275998
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: DAS, Debopriya
: APPLICANT: REDDY, Roopa
: APPLICANT: YAO, Monique G.
: APPLICANT: NGUYEN, Dannel B.
: APPLICANT: LU, Yan
: APPLICANT: TRIBOULEY, Catherine M.
: APPLICANT: YUE, Henry
: APPLICANT: KHAN, Farrah A.
: APPLICANT: GANDHI, Ameena R.
: APPLICANT: AU-YOUNG, Janice
: APPLICANT: LAL, Preeti
: APPLICANT: KEARNEY, Liam
: APPLICANT: ELLIOTT, Vicki S.
: APPLICANT: DING, Li
: APPLICANT: THORNTON, Michael
: TITLE OF INVENTION: LIPID METABOLISM ENZYMES
: FILE REFERENCE: PI-0095 USN
: CURRENT APPLICATION NUMBER: US/10/275,998
: PRIOR FILING DATE: 2002-11-08
: PRIOR APPLICATION NUMBER: US 01/15210
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US 60/203,511
: PRIOR FILING DATE: 2000-05-11
: PRIOR APPLICATION NUMBER: US 60/207,903
: PRIOR FILING DATE: 2000-05-25
: PRIOR APPLICATION NUMBER: US 60/210,150
: PRIOR FILING DATE: 2000-06-07
: PRIOR APPLICATION NUMBER: US 60/213,392
: PRIOR FILING DATE: 2000-06-23
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PERL Program
: SEQ ID NO 7
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 7473224CB1
US-10-275-998-7

Query Match 100.0%; Score 507; DB 6; Length 2270;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAGAAGTCTTTCACCGTGGCCATCCTTGTCTGGCAGCGTTCTGTCCACAGCTCACGGC	60
Db	222	ATGAAGAAGTCTTTCACCGTGGCCATCCTTGTCTGGCAGCGTTCTGTCCACAGCTCACGGC	281
Qy	61	AGCTGCTCAACCTGAAGGCCATGGTGAGGCCGTACAGGAGGAGGCGCATCTGTCC	120
Db	282	AGCTGCTCAACCTGAAGGCCATGGTGAGGCCGTACAGGAGGAGGCGCATCTGTCC	341
Qy	121	TTCTGGGGCTACGGTTGCTACTCTGGGCTGGGGGGCCGTGGCCACGCCAAGTAGAGTG	180
Db	342	TTCTGGGGCTACGGTTGCTACTCTGGGCTGGGGGGCCGTGGCCACGCCAAGTAGAGTG	401
Qy	181	GACTGGTGTGCACGGCCACGACTGCTACTACAGGAACCTTTTGACCAAGGCTGTAC	240
Db	402	GACTGGTGTGCACGGCCACGACTGCTGTACAGGAACCTTTTGACCAAGGCTGTAC	461
Qy	241	CCCTATGTGGACCACTATGATCATCACCATCGAAGAACACTGAGATGCTCTCAGTAGAC	300
Db	462	CCCTATGTGGACCACTATGATCATCACCATCGAAGAACACTGAGATGCTCTCAGTAGAC	521
Qy	301	CTCAACAAGACAGAGTGTGAACAGCAGACATCATGTGTGACAGACATGGTCTGTGTC	360
Db	522	CTCAACAAGACAGAGTGTGAACAGCAGACATCATGTGTGACAGACATGGTCTGTGTC	581
Qy	361	CTCATGAACACAGAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGCG	420
Db	582	CTCATGAACACAGAGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGCG	641
Qy	421	CCACGCCCACTACGACATCTATGAACCGCCCTGAGGAGGTCACTTCAGTCACCA	480
Db	642	CCACGCCCACTACGACATCTATGAACCGCCCTGAGGAGGTCACTTCAGTCACCA	701
Qy	481	TCCCAGCGCCCCCGCCCTCCCTAG	507
Db	702	TCCCAGCGCCCCCGCCCTCCCTAG	728

```

, RESULT 2
PCT-US02-21338-79
; Sequence 79, Application PC/TUS0221338
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330PC
; CURRENT APPLICATION NUMBER: PCT/US02/21338
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21338-79

```

Db	249	ATGAAGAAGTTCTTACCGTGGCCATCCTTGCTGCGACGGTCTGTGCCACAGCTCAGCGC	308
QY	61	AGCGTGCTCAACCTGAAGCCATGGTGGAGCCCGTACAGGGAGGAGCGCATCTGTGTC	120
Db	309	AGCGTGCTCAACCTGAAGCCATGGTGGAGCCCGTACAGGGAGGAGCGCATCTGTGTC	368
QY	121	TTCTGGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGCCCAAGGATGAGGTG	180
Db	369	TTCTGGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGCCCAAGGATGAGGTG	428
QY	181	GACTGGTGCTGCCAGGCCACGACTGCTGTGTACAGGAACTCTTTGACCAGGCTGTAC	240
Db	429	GACTGGTGCTGCCAGGCCACGACTGCTGTGTACAGGAACTCTTTGACCAGGCTGTAC	488
QY	241	CCCTATGTGGACCACTATGATCACACCATCGAGAAACAACACTGAGATAGTCTCAGTGAC	300
Db	489	CCCTATGTGGACCACTATGATCACACCATCGAGAAACAACACTGAGATAGTCTCAGTGAC	548
QY	301	CTCAACAAGACAGAGTGTGACAGCAGACATGTCATGTGTGACAAGAACATGTTCTGTGC	360
Db	549	CTCAACAAGACAGAGTGTGACAGCAGACATGTCATGTGTGACAAGAACATGTTCTGTGC	608
QY	361	CTCATGACCAAGAGCTACCGAGAGGAGTACCGTGGCTTCTCAATGCTACTGCCAGGGC	420
Db	609	CTCATGACCAAGAGCTACCGAGAGGAGTACCGTGGCTTCTCAATGCTACTGCCAGGGC	668
QY	421	CCACGCCCAACTCGACGATCTATGAACCGCCCGCTGAGGAGTCACTGTCAGTCAACAA	480
Db	669	CCACGCCCAACTCGACGATCTATGAACCGCCCGCTGAGGAGTCACTGTCAGTCAACAA	728
QY	481	TCCCGACGGCCCCCGCCCTCCCTAG 507	
Db	729	TCCCGACGGCCCCCGCCCTCCCTAG 755	
RESULT 3			
US-10-188-832-79			
; Sequence 79, Application US/10188832			
; GENERAL INFORMATION:			
; APPLICANT: Mack, David H.			
; APPLICANT: Aziz, Natasha			
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions			
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder			
; TITLE OF INVENTION: Cancer			
; FILE REFERENCE: 018501-002330US			
; CURRENT APPLICATION NUMBER: US/10/188,832			
; CURRENT FILING DATE: 2002-11-22			
; PRIOR APPLICATION NUMBER: US 60/302,814			
; PRIOR FILING DATE: 2001-07-03			
; PRIOR APPLICATION NUMBER: US 60/310,099			
; PRIOR FILING DATE: 2001-08-03			
; PRIOR APPLICATION NUMBER: US 60/343,705			
; PRIOR FILING DATE: 2001-11-08			
; PRIOR APPLICATION NUMBER: US 60/350,666			
; PRIOR FILING DATE: 2001-11-13			
; PRIOR APPLICATION NUMBER: US 60/372,246			
; PRIOR FILING DATE: 2002-04-12			
; NUMBER OF SEQ ID NOS: 207			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 79			
; LENGTH: 2297			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-188-832-79			
Query Match 100.0%; Score 507; DB 6; Length 2297;			
Best Local Similarity 100.0%; Pred. No. 7.3e-133;			
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps			
QY	1	ATGAAGAAGTTCTTACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC	60

Db 117 GGGAAATGCCATCTCTCTACTGGCCCTAGGCTGTCACTGGGACTAGGTGGCAGA 176
QY 160 GGGCAAGCCCAAGATGAGTGGTGTCTGCCACGCCACGACTGTCTTACAGGAA 219
Db 177 GGGCAAGCCCAAGATGAGTGGTGTCTGCCACGCCACGACTGTCTTACAGGAA 236
QY 220 CTCTTTGACCAAGGTTGTCACCCCTATGTGGACCACTATGATCACCACATCGAACAAC 279
Db 237 CTGAAGACCCAGGGTGCAGCATCTACAGGACTATTACAGATACAATT-----TTCC 290
QY 280 ACTGATGATGTGTCAGTGACCTCAACAAGACAGAGTGTGACAAAGCAGACATGTCATGT 339
Db 291 CAGGGGAACATCCATGCTCTGACAAGGAAGTGGTGTGACGACGAGCTGTGTGCTGT 350
QY 340 GACAAAGAACATGGTCTGTGGCTCATGAACAGCAGGATCCAGAGGAGTACCG 392
Db 351 GACAGGAGGTGGCTTCTGCTGAGCGCAACCTGGACACCTACCAAGAGCG 403

RESULT 9

US-10-131-813A-533

; Sequence 533, Application US/10131813A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C139

; CURRENT APPLICATION NUMBER: US/10/131,813A

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; SEQ ID NO 533

; LENGTH: 496

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-813A-533

Query Match 18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCCACAGCTCAGCGGACGCTGCTCAACCTGGAAGGCCATGGTGGAGCGGCTCACA 99
Db 68 GGTGTGATTCCAAATCCAGGGGGGATCTCTGAACCTGGAACAGTGGTCAAGCAAGTCACT 127
QY 100 GGGAGGAGCGGCTCCT 159
Db 128 GGGAAATGCCCCT 187
QY 160 GGGCAGGCGCAAGGATGAGGTGGACTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 219
Db 188 GGGCAACCCCAAGATGCCACGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 247
QY 220 CTCTTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACCACAT 269
Db 248 CTGAAGACCCAGGGGTGGCGCATCTACAAGGACAACAACAAAGCAGCAT 297

RESULT 10

US-10-131-819A-533

; Sequence 533, Application US/10131819A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C134

; CURRENT APPLICATION NUMBER: US/10/131,819A

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

```
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-819A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCACAGCTCAGCGGAGCTGCTCAACCTGAAGGCCATGGTGGAGCGCGTCACA 99
Db 68 GGTGTGATTCCAAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127
QY 100 GGGAGAGCGCCATCCTGCTTCCTGCTGGGCTACGGTTGCTTACTGCTGGGCGCGCT 159
Db 128 GGGAAATGCCCATCCTCTCTTACTGGCCCTACGGCTGTCTACTGGGACTAGGTGGCAGA 187
QY 160 GGCACGCCCAAGGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 219
Db 188 GGCACGCCCAAGGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 247
QY 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCAT 269
Db 248 CTGAAGACCCAGGGGTGGCGCATCTACAAGGACAAACAAGAGCAGCAT 297

RESULT 12
US-10-131-823A-533
; Sequence 533, Application US/10131823A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C126
; CURRENT FILING DATE: 2002-04-24
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-819A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 40 GTTCTGTCACAGCTCAGCGGAGCTGCTCAACCTGAAGGCCATGGTGGAGCGCGTCACA 99
Db 68 GGTGTGATTCCAAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACT 127
QY 100 GGGAGAGCGCCATCCTGCTTCCTGCTGGGCTACGGTTGCTTACTGCTGGGCGCGCT 159
Db 128 GGGAAATGCCCATCCTCTCTTACTGGCCCTACGGCTGTCTACTGGGACTAGGTGGCAGA 187
QY 160 GGCACGCCCAAGGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 219
Db 188 GGCACGCCCAAGGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 247
QY 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCAT 269
Db 248 CTGAAGACCCAGGGGTGGCGCATCTACAAGGACAAACAAGAGCAGCAT 297

RESULT 11
US-10-131-823A-533
; Sequence 533, Application US/10131823A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C143
; CURRENT FILING DATE: 2002-04-24
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
```


us-09-975-456b-1.rnnpn

Mon Feb 10 11:35:49 2003

```

; FILE REFERENCE: P3330R1C138
; CURRENT FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-125-926A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 40 GTTCTGTCCACAGCTCAGCGCAGCTGCTCAACCTGAAGGCCATGGTGGAGGCCGCTCACA 99
Db 68 GGTGTGATTCCAAATCCAGGGGGGATGCTCAACCTGAACAGATGCTCAAGCAAGTGACT 127
Qy 100 GGGAGGAGCGCCATCCCTCTCTTGTGGGCTACGGTTGCTACTGTGGTGGGGCCGT 159
Db 128 GGGAAATGCCCCATCTCTCTACTAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Qy 160 GGGCAAGCCCAAGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
Db 188 GGGCAAGCCCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 247
Qy 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCAT 269
Db 248 CTGAAGACCCAGGGGTGGGCATCTTACAAGGACAAACAACAAAGCAGCAT 297

```

Search completed: February 8, 2003, 06:42:46
Job time : 185 secs

```

; FILE REFERENCE: P3330R1C138
; CURRENT FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-131-829A-533

Query Match      18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 40 GTTCTGTCCACAGCTCAGCGCAGCTGCTCAACCTGAAGGCCATGGTGGAGGCCGCTCACA 99
Db 68 GGTGTGATTCCAAATCCAGGGGGGATGCTCAACCTGAACAGATGCTCAAGCAAGTGACT 127
Qy 100 GGGAGGAGCGCCATCCCTCTCTTGTGGGCTACGGTTGCTACTGTGGGCTGGGGCCGT 159
Db 128 GGGAAATGCCCCATCTCTCTACTAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Qy 160 GGGCAAGCCCAAGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
Db 188 GGGCAAGCCCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 247
Qy 220 CTCCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCAT 269
Db 248 CTGAAGACCCAGGGGTGGGCATCTTACAAGGACAAACAACAAAGCAGCAT 297

```

RESULT 15
US-10-125-926A-533
; Sequence 333, Application US/10125926A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:56 : Search time 143 Seconds
(without alignments)
757.449 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence:

1 MKKFTVAILAGSVLSTAHG.....EPPEVTCSHQSPAPP 168

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pap.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pap.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pap.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pap.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pap.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pap.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pap.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pap.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pap.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pap.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pap.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pap.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pap.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pap.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pap.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pap.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pap.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pap.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pap.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pap.*
21: /cgn2_6/ptodata/1/paa/US097_COMB.pap.*
22: /cgn2_6/ptodata/1/paa/US098_COMB.pap.*
23: /cgn2_6/ptodata/1/paa/US099_COMB.pap.*
24: /cgn2_6/ptodata/1/paa/US100_COMB.pap.*
25: /cgn2_6/ptodata/1/paa/US101_COMB.pap.*
26: /cgn2_6/ptodata/1/paa/US102_COMB.pap.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	168	23	US-09-975-456B-2
2	957	100.0	211	27	US-60-203-511-2
3	957	100.0	211	27	US-60-403-468-4
4	950	99.3	168	25	US-10-104-047-3735
5	895.5	93.6	275	27	US-60-212-356-145
6	892.5	93.3	248	27	US-60-212-356-180

7	892.5	93.3	248	27	US-60-229-525-298	Sequence 298, App
8	892.5	93.3	248	27	US-60-229-525-451	Sequence 451, App
9	747	78.1	168	21	US-09-791-537-148869	Sequence 148869
10	733	76.6	126	27	US-60-229-525-468	Sequence 468, App
11	460	48.1	85	27	US-60-234-446-626	Sequence 626, App
12	353	36.9	145	1	PCT-US01-10542-17	Sequence 17, Appl
13	353	36.9	145	23	US-09-969-384-17	Sequence 17, Appl
14	353	36.9	145	23	US-09-975-456B-7	Sequence 7, Appl
15	352	36.8	145	1	PCT-US01-13529A-6	Sequence 6, Appl
16	352	36.8	145	15	US-09-181-317-1	Sequence 1, Appl
17	352	36.8	145	15	US-09-791-537-140100	Sequence 1, Appl
18	352	36.8	145	22	US-09-835-996A-6	Sequence 6, Appl
19	352	36.8	145	22	US-09-856-486-27	Sequence 27, Appl
20	352	36.8	150	1	PCT-US00-35017A-1342	Sequence 1342, Ap
21	344.5	36.0	144	21	US-09-791-537-148830	Sequence 148830,
22	344.5	36.0	144	21	US-09-856-486-14	Sequence 14, Appl
23	344	35.9	299	27	US-60-212-356-144	Sequence 144, App
24	344	35.9	299	27	US-60-229-525-452	Sequence 452, App
25	340.5	35.6	134	27	US-60-207-316-109	Sequence 109, App
26	319.5	33.4	138	21	US-09-791-537-21221	Sequence 21221, A
27	313.5	32.8	142	21	US-09-791-537-148806	Sequence 148806,
28	312	32.6	118	21	US-09-791-537-131157	Sequence 131157,
29	309.5	32.3	138	21	US-09-791-537-78689	Sequence 78689, A
30	309	32.3	142	21	US-09-791-537-15988	Sequence 15988, A
31	309	32.3	154	23	PCT-US02-23913-325	Sequence 325, App
32	302.5	31.6	144	1	PCT-US02-383-10	Sequence 10, Appl
33	302.5	31.6	144	4	US-08-046-383-10	Sequence 37, Appl
34	302.5	31.6	144	4	US-08-091-941-37	Sequence 37, Appl
35	302.5	31.6	144	8	US-08-463-958-37	Sequence 37, Appl
36	302.5	31.6	144	10	US-08-651-405-37	Sequence 37, Appl
37	302.5	31.6	144	21	US-09-791-537-4717	Sequence 4717, Ap
38	302.5	31.6	144	23	US-09-975-456B-6	Sequence 6, Appl
39	302.5	31.6	144	25	US-10-116-275-269	Sequence 269, App
40	302.5	31.6	144	26	US-10-205-823-325	Sequence 325, App
41	302.5	31.6	164	1	PCT-US00-05988-1010	Sequence 1010, Ap
42	302.5	31.6	164	13	US-08-973-602-29	Sequence 29, Appl
43	302.5	31.6	164	20	US-09-646-777A-246	Sequence 246, App
44	302.5	31.6	164	23	US-09-925-300-1010	Sequence 1010, Ap
45	298.5	31.2	122	21	US-09-791-537-139699	Sequence 139699,

ALIGNMENTS

RESULT 1
US-09-975-456B-2
; Sequence 2, Application US/09975456B
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-2

Query Match 100.0%; Score 957; DB 23; Length 168;
Best Local Similarity 100.0%; Pred. No. 4.2e-85;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKFTVAILAGSVLSTAHGSLNLKANVEAVTGRSAILSVGCGYCGGCGQPKDEV 60
|||||
Db 1 MKKFTVAILAGSVLSTAHGSLNLKANVEAVTGRSAILSVGCGYCGGCGGCGQPKDEV 60
|||||

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTTVAIIAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 DB 44 MKKFTTVAIIAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
 QY 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 DB 104 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 163
 QY 121 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 168
 DB 164 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 211

RESULT 4

US-10-104-047-3735
 ; Sequence 3735, Application US/10104047
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; PRIOR FILING DATE: 2002-03-25
 ; CURRENT FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3735
 ; LENGTH: 168
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 99.3%; Score 950; DB 25; Length 168;
 Best Local Similarity 99.4%; Pred. No. 2e-84;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKFTTVAIIAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 DB 1 MKKFTTVAIIAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 QY 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 DB 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 QY 121 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 168
 DB 121 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 168

RESULT 5

US-60-212-356-145
 ; Sequence 145, Application US/60212356
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CL000677
 ; CURRENT APPLICATION NUMBER: US/60/212,356
 ; CURRENT FILING DATE: 2000-06-19
 ; NUMBER OF SEQ ID NOS: 411
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 145
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 93.6%; Score 895.5; DB 27; Length 275;
 Best Local Similarity 87.7%; Pred. No. 7.8e-79;
 Matches 164; Conservative 1; Mismatches 3; Indels 19; Gaps 3;

QY 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 DB 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 QY 121 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 168
 DB 121 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 168

RESULT 2

US-60-203-511-2
 ; Sequence 2, Application US/60203511
 ; GENERAL INFORMATION:
 ; APPLICANT: Das, Debopriya
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Yao, Monique G.
 ; APPLICANT: Nguyen, Daniel B.
 ; APPLICANT: Lu, Yan
 ; APPLICANT: Tribouley, Catherine M.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Khan, Farrah A.
 ; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
 ; FILE REFERENCE: PI-0095 P
 ; CURRENT APPLICATION NUMBER: US/60/203,511
 ; CURRENT FILING DATE: 2000-05-11
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 100.0%; Score 957; DB 27; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5.4e-85;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTTVAIIAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
 DB 44 MKKFTTVAIIAGSVLSTAGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
 QY 61 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
 DB 104 DMCCHAHDCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 163
 QY 121 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 168
 DB 164 LMNQTYREYRGFLNVYCGQPTPNCISYEPPEEVTCSHQSPPAPP 211

RESULT 3

US-60-403-468-4
 ; Sequence 4, Application US/60403468
 ; GENERAL INFORMATION:
 ; APPLICANT: Silos-Santiago, Immaculada
 ; TITLE OF INVENTION: Methods and compositions for treating
 ; TITLE OF INVENTION: urological disorders using 260, 55089 or 21407
 ; FILE REFERENCE: MP102-148P1(M)
 ; CURRENT APPLICATION NUMBER: US/60/403,468
 ; CURRENT FILING DATE: 2002-08-14
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: homosapiens
 ; OTHER INFORMATION: Incyte ID No: 7473224CD1

Query Match 100.0%; Score 957; DB 27; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5.4e-85;

Qy	1	KKKFFTVAILAGSVLSTAHGSLNLKAMVAVTGRSAILSFVGYCCYCGLGGRGQPKDEV	60
Db	44	KKKFFTVAILAGSVLSTAHGSLNLKAMVAVTGRSAILSFVGYCCYCGLGGRGQPKDEV	103
Qy	61	DKCCHAHGCCQBELFDGCGHPYVDHYDHTIENNTETVCSDLNKTCEQKQTCMCDKNWVLC	120
Db	104	DKCCHAHGCCQBELFDGCGHPYVDHYDHTIENNTETVCSDLNKTCEQKQTCMCDKNWVLC	163
Qy	121	LNQNTYREYRGFLNVYCOGPTNCISIYPPPEEV-----TC-----SHQSPAPPA	166
Db	164	LNQNTYREYRGFLNVYCOGPTNCISIYPPPEEVHLLFTLTCPSLNSGSAASTEPAPPA	223
Qy	167	-----pp 168	
Db	224	RKPLKPP 230	

RESULT 6

```

US-60-212-356-180
; Sequence 180, Application US/60212356
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00677
; CURRENT APPLICATION NUMBER: US/60/212,356
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 248
; TYPE: PRT
; ORGANISM: HUMAN
US-60-212-356-180

```

Query Match	93.3%	Score 892.5;	DB 27;	Length 248;
Best Local Similarity	94.6%;	Pred. No. 1.4e-78;		
Matches 159;	Conservative 2;	Mismatches 6;	Indels 1;	Gaps 1;
QY	1	KKKFTTVAIIAGSVLSTAHGSLLLKAWFVAVTGRSAILSFVGYGCGYCGLGGRGQPKDEV	60	
Db	44	KKKFTTVAIIAGSVLSTAHGSLLLKAWFVAVTGRSAILSFVGYGCGYCGLGGRGQPKDEV	103	
QY	61	DMCCHAHCCCYQLFDGCGHPYVDHYDHTIENNTETVCSDLNKTECDKOTCMCDKNMVL	120	
Db	104	DMCCHAHCCCYQLFDGCGHPYVDHYDHTIENNTETVCSDLNKTECDKOTCMCDKNMVL	163	
QY	121	LMNQTYREYRGFLNVYCGQPTNCISYEPPPEVTCSHQSPAPP	168	
Db	164	LMNQTYREYRGFLNVYCGQPTNCISYEPPPEVSGEDTVPASP	210	

RESULT 7

```

US-60-229-525-298
; Sequence 298, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 298
; LENGTH: 248
; TYPE: PRT
; ORGANISM: HUMAN
US-60-229-525-298

```

Query Match	93.3%;	Score 892.5;	DB 27;	Length 248;
Best Local Similarity	94.6%;	Pred. No. 1.4e-78;		
Matches 159;	Conservative 2;	Mismatches 6;	Indels 1;	Gaps
QY	1	MKKFTFVAILAGSVLSTAHSLLNLKAMVEAVTGRSAILS	SFVGVCYCGLGGRGQPDEV	60
Dd	44	MKKFTFVAILAGSVLSTAHSLLNLKAMVEAVTGRSAILS	SFVGVCYCGLGGRGQPDEV	103
QY	61	DWCCHADCCYOELFDQGCHPYVDHYDHTTENNTIEI	VCSDLNTECDKOTCMCKNNVL	120
Dd	104	DWCCHADCCYOELFDQGCHPYVDHYDHTTENNTIEI	VCSDLNTECDKOTCMCKNNVL	163
QY	121	LNMNTYREEYRGFLUNVYCQGTPTNCSTIYEPPDEVT	CSSHQSAPPAPP	168
Dd	164	LNMNTYREETGFGLUNVYCQGTPTNCSTIYEPPDEVS	-GDTVFVPASP	210

RESULT 8

```

RES001 8
US-60-229-525-451
; Sequence 451, Application US/60229525
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000772
; CURRENT APPLICATION NUMBER: US/60/229,525
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 819
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 451
; LENGTH: 248
; TYPE: PRT
; ORGANISM: HUMAN
US-60-229-525-451

```

```

Query Match          93.3%; Score 892.5; DB 27; Length 248;
Best Local Similarity 94.6%; pred. No. 1.4e-78;
Matches 159; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY      1  MKKFFTVALLAGSVLSTAHGSLLLNKAMWEAVTGRSAILSFVGYGCGYCLGGRGQPKDEV 60
      Db      |||
      44  MKKFFTVALLAGSVLSTAHGSLLLNKAMWEAVTGRSAILSFVGYGCGYCLGGRGQPKDEV 103
      QY      61  DMCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTIEIVCSDLNKTECDKQTCMCDNNVLC 120
      Db      |||
      104  DMCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTIEIVCSDLNKTECDKQTCMCDNNVLC 163
      QY      121  LMNQTYREYRGFLNVYCGQTPNCSTIYEPDPPEVTCSHQSPAPPAPP 168
      Db      |||
      164  LMNQTYREYRGFLNVYCGQTPNCSTIYEPDPPEVTS-GEDTVTPASP 210

```

RESULT 9

```

RESOLVER
US-09-791-537-148869
; Sequence 148869, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 148869
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-148869

```

Mon Feb 10 11:36:16 2003

Best Local Similarity 98.8%; Pred. No. 8.8e-37;
Matches 79; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 78.1%; Score 747; DB 21; Length 168;

Best Local Similarity 75.2%; Pred. No. 1.5e-64;

Matches 124; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKKFFVATLSTAGSLSTAGSLNLKAMVEAVTGRSAILSFVGYGCGGLGGGRGQPKDEV 60

DB 1 MKKFFAIVLAGSVVTAHSSLLNLKSMVEATHRNSILSFVGYGCGGLGGGRHPDEV 60

QY 61 DMCHAHDCYQELFDQGGHPYVDHYDHTIENNTIENNVCSLNTKTECDKOTCMCDKNMVL 120

DB 61 DMCHAHDCYQELFDQGGHPYVDHYDHTIENNTIENNVCSLNTKTECDKOTCMCDKSLTLC 120

QY 121 LMNQTREYRGFLNVCYCGPNCISYPPPEVTCSHQSPAPP 165

DB 121 LKDHPRNRYGYNVICOGPTPNCISYPPPEVTCGHGLPATP 165

RESULT 10

US-60-229-525-468

; Sequence 468, Application US/60229525

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE

; TITLE OF INVENTION: PROTEINS, AND USES THEREOF

; FILE REFERENCE: CL000772

; CURRENT APPLICATION NUMBER: US/60/229,525

; CURRENT FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 819

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 468

; LENGTH: 126

; TYPE: PRT

; ORGANISM: HUMAN

US-60-229-525-468

Query Match 76.6%; Score 733; DB-27; Length 126;

Best Local Similarity 100.0%; Pred. No. 2.6e-63;

Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GLLNLKAMVEAVTGRSAILSFVGYGCGGLGGGRGQPKDEVDMCHAHDCYQELFDQGC 79

DB 1 GLLNLKAMVEAVTGRSAILSFVGYGCGGLGGGRGQPKDEVDMCHAHDCYQELFDQGC 60

QY 80 HPYVDHYDHTIENNTIENNVCSLNTKTECDKOTCMCDKNMVLCLMNAQTYREYRGFLNVCY 139

DB 61 HPYVDHYDHTIENNTIENNVCSLNTKTECDKOTCMCDKNMVLCLMNAQTYREYRGFLNVCY 120

QY 140 GTPPNC 145

DB 121 GTPPNC 126

RESULT 11

US-60-234-446-626

; Sequence 626, Application US/60234446

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL000832

; CURRENT APPLICATION NUMBER: US/60/234,446

; CURRENT FILING DATE: 2000-09-18

; NUMBER OF SEQ ID NOS: 1797

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 626

; LENGTH: 85

; TYPE: PRT

; ORGANISM: HUMAN

US-60-234-446-626

Query Match 48.1%; Score 460; DB 27; Length 85;

Best Local Similarity 98.8%; Pred. No. 8.8e-37;
Matches 79; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 21 SLLNLKAMVEAVTGRSAILSFVGYGCGGLGGGRGQPKDEVDMCHAHDCYQELFDQGC 80

DB 1 SLLNLKAMVEAVTGRSAILSFVGYGCGGLGGGRGQPKDEVDMCHAHDCYQELFDQGC 60

QY 81 PYVDHYDHTIENNTIENNVCSL 100

DB 61 PYVDHYDHTIENNTIENNVCSL 80

RESULT 12

PCT-US01-10542-17

; Sequence 17, Application PC/TUS0110542

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Gene Sequence Polynucleotides, Polypeptides, and Antibod

; FILE REFERENCE: PT055PCT

; CURRENT APPLICATION NUMBER: PCT/US01/10542

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 60/236,384

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/194,118

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-10542-17

Query Match 36.9%; Score 353; DB 1; Length 145;

Best Local Similarity 45.5%; Pred. No. 5e-26;

Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VALLAGSVLSTA---HGSLNLKAMVEAVTGRSAILSFVGYGCGGLGGGRGQPKDEVDM 62

DB 3 LALLCGIVVMAGVPIQGGLILNLKMKVQVTKMPLSYWPGYCHGCGGLGGGRGQPKDATDW 62

QY 63 CCHAHDCYQELFDQGGHPYVDHYDHTIENNTIENNVCSLNTKTECDKOTCMCDKNMVLCLM 122

DB 63 CQOHDCCYDHLKIQGCSIYKDYRYNFSQ-NIHCS-D-KGSWCEQQLCACDKEVAFCLK 120

QY 123 N-QTYREYRGFLNVCYCGPTPNC 145

DB 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145

RESULT 13

US-09-969-384-17

; Sequence 17, Application US/09969384

; GENERAL INFORMATION:

; APPLICANT: Moore, et al.

; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies

; FILE REFERENCE: PT055P1

; CURRENT APPLICATION NUMBER: US/09/969,384

; CURRENT FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: PCT/US01/10542

; PRIOR FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 60/236,384

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/194,118

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-969-384-17

Query Match	36.9%;	Score 353;	DB 23;	Length 145;
Best Local Similarity	45.5%;	Pred. No. 5e-26;		
Matches	66;	Conservative 19;	Mismatches 52;	Indels 8; Gaps 4;
7	VAILAGSVLSTA----	HGSLNLNLKANVEAVTGRSAITLSFVGYCGGLGGRGQPKDEVDW	62	
	: : : : :	: : : : :	: : : : :	: : : : :
3	LALLCGULVWAGVIPTGGGLFLNLKNKVKQTKMPILSYWPYCGHGLGGRGQPKDATDW	62		
	: : : : :	: : : : :	: : : : :	: : : : :
63	CCHADHCCYOELFDQGHVVDHYDHTIENNTFIVCSDLNKTECDKQTCMDCKNNVLCLM	122		
	: : : : :	: : : : :	: : : : :	: : : : :
63	CCQTHDCCYDLHKTQGSYIKDYRYNFSGQ-NIHCSQ-KGSWCQQQLCACDKEVAFCLK	120		
	: : : : :	: : : : :	: : : : :	: : : : :
123	N--QTYREYRGFLNYVCGQPTPNC	145		
	: : : : :	: : : : :	: : : : :	: : : : :
121	RNLDTYQKRLRFYWRPHRCRGTPGC	145		
	: : : : :	: : : : :	: : : : :	: : : : :

Query Match	36.9%	Score 353	DB 23	Length 145
Best Local Similarity	45.5%	Pred. No. 5e-26		
Matches	66	Conservative 19	Mismatches 52	Indels 8
Gaps	4			
QY	7	VALLAGSVLSTA----	HGSLNLNKAMVEAVTGRSAILSFEVGYCGGLGGRRQPKDEVDW	62
Db		: : : : : :	: : : : : :	
	3	LALLCGLVVMAGVIP	IOGGILNLNKNVKQVTGMPILSYWPYCGHCGLLGGRRQPKDADTW	62
QY	63	CCAHNDCCYQLEDFG	CGHPYVDYDHTIENNTIIVCSDLNKTCCDKQTCMCDKNMVLCLM	122
Db		: : : : : :	: : : : : :	
	63	CCQTHDCCYDHLKTG	CSYKDYIRYFNFSOG-NIHCSD-KGSWCQQLCACDKEVAFCLK	120
QY	123	N--QTYREYRGFLNVY	CQGPTPNC	145
Db		: : : : : :	: : : : : :	
	121	RNLDTYQRLRFYWRP	HCRGOTGCG	145

```

; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-12529A-6

```

Query Match	36.8%	Score 352;	DB 1;	Length 145;
Best Local Similarity	45.5%	Pred. No. 6.2e-26;		
Matches 66;	Conservative 19;	Mismatches 52;	Indels 8;	Gaps 4;
QY	7	VAILAGSVLSTA----	HGSLNLNKAMVEAVTGT	RAILSVFYGYCYGLGRRGQPKDEVDW 62
		: : : : : :	: : : : : :	: : : : : :
Db	3	LALLUGLIVWAGVTP	IOGGLNLNLMKVQV	TGKMPILSYWPYCYGCHGLGRRGQPKDADW 62
		: : : : : :	: : : : : :	: : : : : :
QY	63	CCHAHDCCYGELF	DQGGCHPVYVDHDT	IENNTETVCSDLNKTBCDKQTCMCDKNVUCLM 122
		: : : : : :	: : : : : :	: : : : : :
Db	63	CCOTHDCCYDHLKT	QCGGIYKYDYRYN	FSOG-NIHSCD-KGSWCEQQLCADCREVAFCLK 120
QY	123	N--QTYREERYRGL	NVYCYGQPTPNC	145
		: : : : : :	: : : : : :	: : : : : :
Db	121	RNLDTYOKRLRFY	WRPHCRGOTPGC	145

Search completed: February 10, 2003, 10:40:26
Job time : 145 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:36:37 ; Search time 22 Seconds
(without alignments)
619.147 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence: 1 MKKFFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 405691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	211	1	PCT-US02-21338-80
2	957	100.0	211	6	US-10-188-832-80
3	957	100.0	211	6	US-10-275-998-2
4	353	36.9	145	1	PCT-US02-29560-363
5	353	36.9	145	5	US-09-949-002-396
6	353	36.9	145	6	US-10-245-882-363
7	353	36.9	145	5	US-09-949-002-514
8	352	36.8	145	6	US-10-276-781-1625
9	273.5	28.6	116	6	US-10-131-813A-534
10	273.5	28.6	116	6	US-10-131-819A-534
11	273.5	28.6	116	6	US-10-131-823A-534
12	273.5	28.6	116	6	US-10-131-824A-534
13	273.5	28.6	116	6	US-10-131-826A-534
14	273.5	28.6	116	6	US-10-131-829A-534
15	273.5	28.6	116	6	US-10-125-926A-534
16	273.5	28.6	116	6	US-10-127-829A-534
17	273.5	28.6	116	6	US-10-127-831A-534
18	273.5	28.6	116	6	US-10-127-835A-534
19	273.5	28.6	116	6	US-10-127-837A-534
20	273.5	28.6	116	6	US-10-127-842A-534
21	273.5	28.6	116	6	US-10-127-850A-534
22	273.5	28.6	116	6	US-10-127-901A-534
23	273.5	28.6	116	6	US-10-128-689A-534
24	273.5	28.6	116	6	US-10-131-830A-534
25	273.5	28.6	116	6	US-10-131-833A-534
26	273.5	28.6	116	6	US-10-131-837A-534

ALIGNMENTS

RESULT 1

PCT-US02-21338-80

; Sequence 80, Application PC/TUS0221338

; GENERAL INFORMATION:

; APPLICANT: Mack, David H.

; APPLICANT: Aziz, Natasha

; TITLE OF INVENTION: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions and Methods of Screening for Modulators of Bladder

; FILE REFERENCE: 018501-002330PC

; CURRENT APPLICATION NUMBER: PCT/US02/21338

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: US 60/302,814

; PRIOR FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: US 60/310,099

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: US 60/343,705

; PRIOR FILING DATE: 2001-11-08

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/372,246

; PRIOR FILING DATE: 2002-04-12

; NUMBER OF SEQ ID NOS: 207

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 80

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US02-21338-80

Query Match

Best Local Similarity 100.08; Score 957; DB 1; Length 211;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKKFFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCVGLGGRCQPKDEV	60
DB	44	MKKFFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCVGLGGRCQPKDEV	103
QY	61	DWCCHAHCCYQELFDQGCCHPYVDHYHTTENNTFVCSDLNKTCDKQTCMCDKNVLC	120
DB	104	DWCCHAHCCYQELFDQGCCHPYVDHYHTTENNTFVCSDLNKTCDKQTCMCDKNVLC	163
QY	121	LMNQTYREYRGFLNVYCOGPTPNCISYIEPPPEVTCSHQSPAPP 168	
DB	164	LMNQTYREYRGFLNVYCOGPTPNCISYIEPPPEVTCSHQSPAPP 211	

RESULT 2

Mon Feb 10 11:36:17 2003

```

US-10-188-832-80
; Sequence 80, Application US/10188832
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-00233005
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 80
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-80

Query Match 100.0%; Score 957; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.1e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
DB 44 MKKFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
QY 61 DMCCHAHDCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCDKNWVLC 120
DB 104 DMCCHAHDCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCDKNWVLC 163
QY 121 LMNQTREYRGFLNVCQGPNCISYIEPPPEVTCSHQSPAPPAPP 168
DB 164 LMNQTREYRGFLNVCQGPNCISYIEPPPEVTCSHQSPAPPAPP 211

RESULT 3
US-10-275-998-2
; Sequence 2, Application US/10275998
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAS, Debopriya
; APPLICANT: REDDY, Roopa
; APPLICANT: YAO, Monique G.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: DING, Li
; APPLICANT: THORNTON, Michael
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0095 USN
; CURRENT APPLICATION NUMBER: US/10/275,998
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 01/15210
; PRIOR FILING DATE: 2001-05-11

```

```

; PRIOR APPLICATION NUMBER: US 60/203,511
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/207,903
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/210,150
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,392
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 7473224CD1
US-10-275-998-2

Query Match 100.0%; Score 957; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.1e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 60
DB 44 MKKFTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 103
QY 61 DMCCHAHDCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCDKNWVLC 120
DB 104 DMCCHAHDCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCDKNWVLC 163
QY 121 LMNQTREYRGFLNVCQGPNCISYIEPPPEVTCSHQSPAPPAPP 168
DB 164 LMNQTREYRGFLNVCQGPNCISYIEPPPEVTCSHQSPAPPAPP 211

RESULT 4
PCT-US02-29560-363
; Sequence 363, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; CURRENT FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 363
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560-363

Query Match 36.9%; Score 353; DB 1; Length 145;
Best Local Similarity 45.5%; Pred. No. 8.3e-28;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEV 62
DB 3 LALLCGLVVMAGVIPIQGGILNLKMKVKQVTGKMPILSTWPTGCHGCGYGLGGRGQPKD 62
QY 63 CCHAHDCCYQELFDQGHYPYVDHYDHTTENNTIIVCSDLNKTCDKQTCMCDKNWVLC 122

```

```
Db 63 CCQTHDCCYDHLKTCGCSIYKDYRYNFSQG-NIHCSO-KGSWCQEQQLCACDKEVAFCLK 120
QY 123 N--QTYREYRGFLNVYCGQPTPNC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTPGC 145

RESULT 5
US-09-949-002-396
; Sequence 396, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-396

Query Match 36.9%; Score 353; DB 5; Length 145;
Best Local Similarity 45.5%; Pred. No. 8.3e-28;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYGCGLGGRGQPKDEVDW 62
Db 3 LALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGCGLGGRGQPKDATDW 62
QY 63 CCHAHDCCYOELFDGCHPYVDHYDHTIENNTTEIVCSDLNKTCDKQTCMCDKNVLCML 122
Db 63 CCQTHDCCYDHLKTCGCSIYKDYRYNFSQG-NIHCSO-KGSWCQEQQLCACDKEVAFCLK 120
QY 123 N--QTYREYRGFLNVYCGQPTPNC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTPGC 145

RESULT 6
US-10-245-882-363
; Sequence 363, Application US/10245882
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezzi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710US
; CURRENT APPLICATION NUMBER: US/10/245,882
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/323,887
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/325,114
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/340,944
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/355,145
```

```
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/355,257
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/369,899
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 363
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-882-363
```

```
Query Match 36.9%; Score 353; DB 6; Length 145;
Best Local Similarity 45.5%; Pred. No. 8.3e-28;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYGCGLGGRGQPKDEVDW 62
Db 3 LALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGCGLGGRGQPKDATDW 62
QY 63 CCHAHDCCYOELFDGCHPYVDHYDHTIENNTTEIVCSDLNKTCDKQTCMCDKNVLCML 122
Db 63 CCQTHDCCYDHLKTCGCSIYKDYRYNFSQG-NIHCSO-KGSWCQEQQLCACDKEVAFCLK 120
QY 123 N--QTYREYRGFLNVYCGQPTPNC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
```

```
RESULT 7
US-09-949-002-514
; Sequence 514, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 514
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-514
```

```
Query Match 36.9%; Score 353; DB 5; Length 157;
Best Local Similarity 45.5%; Pred. No. 9e-28;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYGCGLGGRGQPKDEVDW 62
Db 15 LALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGCGLGGRGQPKDATDW 74
QY 63 CCHAHDCCYOELFDGCHPYVDHYDHTIENNTTEIVCSDLNKTCDKQTCMCDKNVLCML 122
Db 75 CCQTHDCCYDHLKTCGCSIYKDYRYNFSQG-NIHCSO-KGSWCQEQQLCACDKEVAFCLK 132
QY 123 N--QTYREYRGFLNVYCGQPTPNC 145
Db 133 RNLDYQKRLRFYWRPHCRGQTPGC 157
```

```
RESULT 8
US-10-276-781-1625
; Sequence 1625, Application US/10276781
```

```

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1625
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-781-1625

Query Match          36.8%; Score 352; DB 6; Length 145;
Best Local Similarity 45.5%; Pred. No. 1e-27;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDM 62
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 3 LALLGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDATDW 62
QY 63 CCHAHDCYQELFDGCHPYVDHYDHTIENNTIEVCSDLNKTCDKQTCMCDKNMVLCLM 122
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 63 CCOTHCDCYDHLKTQGGIYKDYRNFSGQ-NIHCSG-KGSWCEQQLCACKEVAFCCLK 120
QY 123 N--QTYREYRGLNVCYCGQPTPC 145
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 121 RNLDYQKRLRYWRPHRCRGQTPGC 145

RESULT 9
US-10-131-813A-534
; Sequence 534, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263

```

```

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1625
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-781-1625

Query Match          36.8%; Score 352; DB 6; Length 145;
Best Local Similarity 45.5%; Pred. No. 1e-27;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDM 62
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 3 LALLGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDATDW 62
QY 63 CCHAHDCYQELFDGCHPYVDHYDHTIENNTIEVCSDLNKTCDKQTCMCDKNMVLCLM 122
   |||:|:|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~
Db 63 CCOTHCDCYDHLKTQGGIYKDYRNFSGQ-NIHCSG-KGSWCEQQLCACKEVAFCCLK 120
QY 123 N--QTYREYRGLNVCYCGQPTPC 145
   ||:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~
Db 121 RNLDYQKRLRYWRPHRCRGQTPGC 145

RESULT 9
US-10-131-813A-534
; Sequence 534, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-819A-534

Query Match 28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

Qy 7 VAILAGSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDW 62
Db 3 LALLGLVVMAGVPIQGILNLKMKVKQVTGKMPILSYWPGCHGCGLGGRGQPKDATDW 62

Qy 63 CCHAHDCCYQELFDGCHPYVDHYDHTIENNTTEIVCSDLNTECDKQTCMCDKNMVLCLM 122
Db 63 CCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCHMDLSQRYC-----LMAVF 105

Qy 123 NQTYRE 128
Db 106 NVIYLE 111

RESULT 11
US-10-131-823A-534
; Sequence 534, Application US/10131823A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C143
; CURRENT APPLICATION NUMBER: US/10/131,823A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-823A-534

Query Match 28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

Qy 7 VAILAGSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDW 62
Db 3 LALLGLVVMAGVPIQGILNLKMKVKQVTGKMPILSYWPGCHGCGLGGRGQPKDATDW 62

Qy 63 CCHAHDCCYQELFDGCHPYVDHYDHTIENNTTEIVCSDLNTECDKQTCMCDKNMVLCLM 122
Db 63 CCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCHMDLSQRYC-----LMAVF 105

Qy 123 NQTYRE 128
Db 106 NVIYLE 111

RESULT 12
US-10-131-824A-534
; Sequence 534, Application US/10131824A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C126
; CURRENT APPLICATION NUMBER: US/10/131,824A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588

```
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-824A-534

Query Match      28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY 7 VAILAGSVLSTA-----HGSLLNLKAMWEAVTGRSAILSFSVGYCYCGLGGRGQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLGGLVVMAGVPIQGGILNLNKKVKQVTGKMPILSYWPGYCHGCGLGGRGQPKDATDW 62

QY 63 CCHAHDCCYQELFDGCHPYVDYDHTIENNTTEIVCSDLNKTCDKQTCMCDKNWVLCIM 122
   || ||||| ||||| ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 63 CCQTHDCCYDHLTKTGGGIYKDN-----NKSSIHCMDSQRYC-----LMAVF 105

QY 123 NOTYRE 128
Db 106 NVIYLE 111
```

```
RESULT 13
US-10-131-826A-534
; Sequence 534, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-534

Query Match      28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY 7 VAILAGSVLSTA-----HGSLLNLKAMWEAVTGRSAILSFSVGYCYCGLGGRGQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLGGLVVMAGVPIQGGILNLNKKVKQVTGKMPILSYWPGYCHGCGLGGRGQPKDATDW 62

QY 63 CCHAHDCCYQELFDGCHPYVDYDHTIENNTTEIVCSDLNKTCDKQTCMCDKNWVLCIM 122
   || ||||| ||||| ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 63 CCQTHDCCYDHLTKTGGGIYKDN-----NKSSIHCMDSQRYC-----LMAVF 105

QY 123 NOTYRE 128
Db 106 NVIYLE 111

RESULT 14
US-10-131-829A-534
; Sequence 534, Application US/10131829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C138
; CURRENT APPLICATION NUMBER: US/10/131,829A
; CURRENT FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
```



```

LENGTH: 116
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-829A-534

Query Match      28.6%; Score 273.5; DB 6; Length 116;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

7 VAIAGSVLSTA---HGSLNLKAMVEAVTGRSATLSFVGYCYGCGLGRGQPKDEVDM 62
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3 LALICGLVWVAGVPIQGGILNLNKKVKQVCKMPLSYWYPYCGHCLGGRGQPKDATDW 62
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 CCHAHDCYQBELFPOGGHPVVDHYDHTIENTIEVCSDLNKTCDKQTCMCDKNMVLCLM 122
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 CCQTHDCYDHLKTQGGCYKDN-----NKSSIHCMDSLQRVC-----LMAVF 105
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

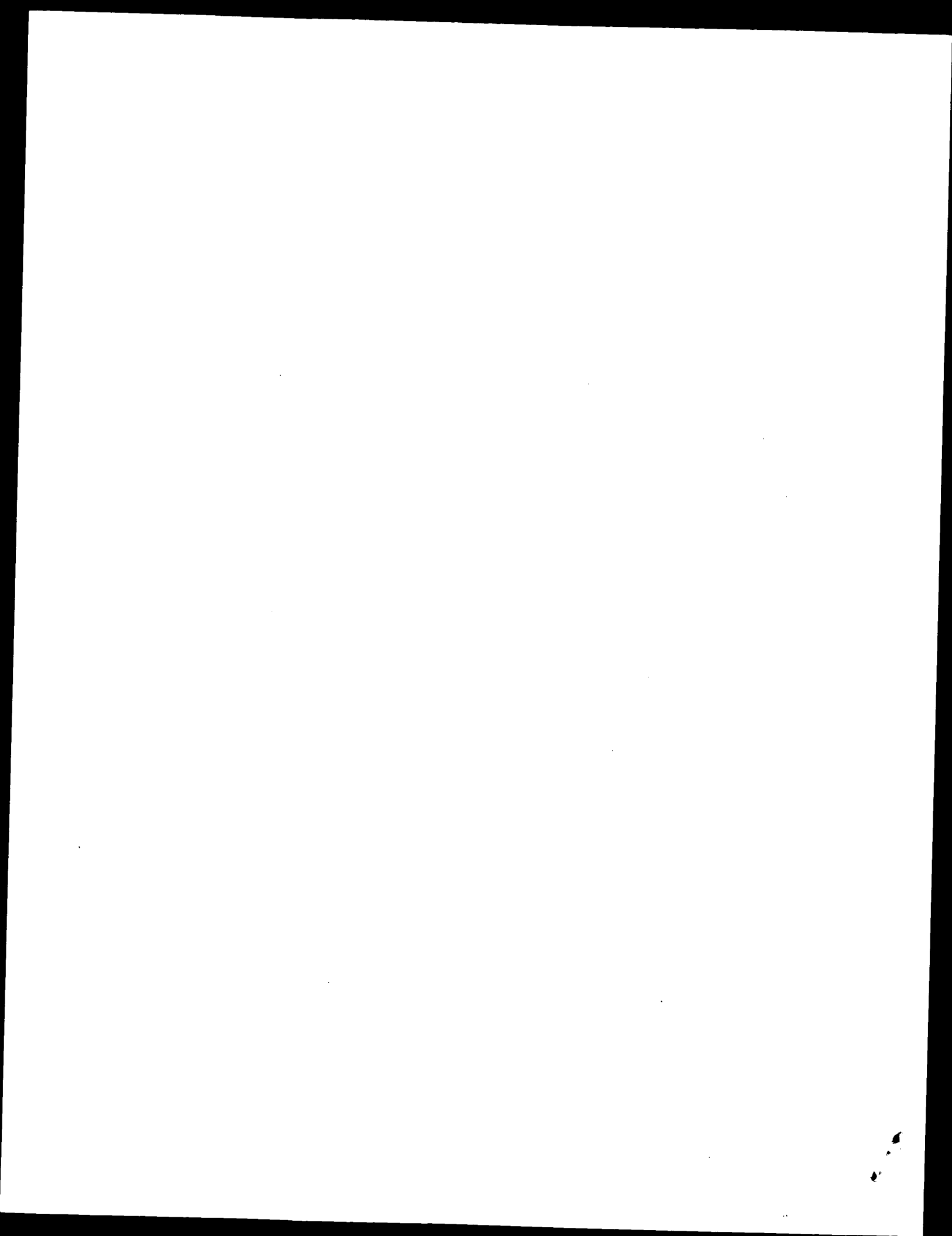
QY      123 NOTYPE 128
DB      106 NVTYPE 111

```

```

RESULT 15
US-10-125-926A-534
; Sequence 534, Application US/10125926A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33301C80
; CURRENT APPLICATION NUMBER: US/10/125,926A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/036974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT

```



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 00:10:29 : Search time 2609 Seconds
(without alignments)
5655.470 Million cell updates/sec

Title: US-09-975-456b-1
Perfect score: 507
Sequence: 1 atgaagaagtcttccacgt.....cgccccccgcctccctccctag 507

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pin.*
35: em.htg_rod.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	507	100.0	507	9	AF306566	Homo sapi
2	507	100.0	2270	6	AX304469	Sequence
3	505.4	99.7	2716	9	AK093645	Homo sapi
4	340.6	67.2	906	10	AF166099	Mus muscu
5	212	41.8	135571	9	HS340N1	298257 Human DNA s
6	148	29.2	98743	9	AL158172	Human DNA
7	135.8	26.8	186589	2	AL844178	Human DNA
8	129.4	25.5	157317	2	AL118094	Mus muscu
9	129.4	25.5	176574	2	AC118094	Rattus no
10	99	19.5	878	9	AF112982	Homo sapi
11	99	19.5	1938	9	AF118625	Homo sapi
12	99	19.5	2747	9	BC025706	Homo sapi
13	95.6	18.9	496	6	AX464400	Sequence
14	93.2	18.4	1445	10	MMU18119	Mus muscu
15	93.2	18.4	1480	10	BC029347	Mus muscu
16	91.2	18.0	157317	2	AC118094	Rattus no
17	88	17.4	4325	6	AR081988	Sequence
18	88	17.4	4325	6	AR198384	Sequence
19	88	17.4	4372	10	RRU07798	Rattus norv
20	87.4	17.2	1913	10	AF162713	Mus muscu
21	84.2	16.6	414	10	MMU66873	Mus muscu
22	84.2	16.6	1986	10	BC030899	Mus muscu
23	82.8	16.3	1803	10	RRU03763	Rattus norv
24	82.8	16.3	1828	6	AR081995	Sequence
25	82.8	16.3	1828	6	AR198391	Sequence
26	82.4	16.3	1233	6	E37214	Mouse secre
27	82.4	16.3	1233	10	AF112983	Mus muscu
28	82.4	16.3	1975	10	AF169407	Mus muscu
29	82.4	16.3	2166	10	AF169408	Mouse secre
30	82	16.2	501	6	E37202	Mouse secre
31	80.8	15.9	904	10	AF124374	Mus muscu
32	76.8	15.1	1014	6	AR081996	Sequence
33	76.8	15.1	1014	6	AR198392	Sequence
34	76.8	15.1	1016	9	HSU03090	Sequence
35	76.8	15.1	1871	9	AK097693	Homo sapien
36	75.8	15.0	742	6	AR105919	Sequence
37	75.8	15.0	742	6	AR211354	Sequence
38	75.8	15.0	1020	9	HSU95301	Human calci
39	71.2	14.0	487	6	BD013155	A gene en
40	71.2	14.0	487	9	AF189279	Homo sapi
41	71.2	14.0	487	23	BD010183	A gene en
42	69.4	13.7	98743	9	AL158172	Human DNA
43	69	13.6	445	5	TMPHA2NEU	X77645 T.mucrosqua
44	69	13.6	776	5	AF408409	Proteobact
45	67.4	13.3	713	5	ACU21335	Agklistrodon

ALIGNMENTS

RESULT 1
AF306566
LOCUS
DEFINITION Homo sapiens group IIF secreted phospholipase A2 mRNA, complete cds.
ACCESSION AF306566
VERSION AF306566.1 GI:12276059
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 507)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Valentin,E., Singer,A.G., Ghomashchi,F., Lazdunski,M., Gelb,M.H.
and Lambeau,G.

TITLE Cloning and recombinant expression of human group IIF-secreted phospholipase A(2)
JOURNAL Biochem. Biophys. Res. Commun. 279 (1), 223-228 (2000)
MEDLINE 20563827
PUBMED 11112443
REFERENCE 2 (bases 1 to 507)
AUTHORS Valentini, E., Lazdunski, M. and Lambeau, G.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) IPMC, CNRS, 660, Route des Lucioles Sophia Antipolis, Valbonne 06560, France
FEATURES
source location/Qualifiers
1..507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p35"
1..507
/codon_start=1
/product="group IIF secreted phospholipase A2"
/protein_id="AAG50242.1"
/db_xref="GI:12276060"
/translation="MKFFTVAILAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGY GCVGLGGRGQPDVDCWCHADHCYQELFDQGHYPVDHYDHTIENITEIVCSDLN KTCDKQTCWCDKRNWVLCNLTQYREYRGFLNVYCGQPTNCSYIEPPPEVTCSHQ SPAPPAP"
BASE COUNT 112 a 162 c 137 g 96 t
ORIGIN
Query Match 100.0%; Score 507; DB 9; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.6e-103;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCTTGTGCGCAGCGTTCTGTCCACAGCTCAGCGC 60
Db 1 ATGAAGAAGTTCTTACCGTGGCCATCTTGTGCGCAGCGTTCTGTCCACAGCTCAGCGC 60
QY 61 AGCGTCTCAACTGAAGGCCATGTGAGGCGCGTCACAGGAGGAGCGCCATCTCTGCC 120
Db 61 AGCGTCTCAACTGAAGGCCATGTGAGGCGCGTCACAGGAGGAGCGCCATCTCTGCC 120
QY 121 TTCGTGGGCTACGGTTGCTTACTGTGGGCTGGGGCGCGTCACAGGAGGAGCGCCATCTCTGCC 180
Db 121 TTCGTGGGCTACGGTTGCTTACTGTGGGCTGGGGCGCGTCACAGGAGGAGCGCG 180
QY 181 GACTGTGTGCGCCACCGCCACGCTGCTCTACAGGAACTCTTTGACCAAGCGCTGTAC 240
Db 181 GACTGTGTGCGCCACCGCCACGCTGCTCTACAGGAACTCTTTGACCAAGCGCTGTAC 240
QY 241 CCTATGTGGACCACTATGATCACCACATCGAGAACACACTGAGATAGTCTGCAGTGAC 300
Db 241 CCTATGTGGACCACTATGATCACCACATCGAGAACACACTGAGATAGTCTGCAGTGAC 300
QY 301 CTCACAAAGACAGAGTGTGACAGCAGACATCATGTGTGACAAAGACATGTTCTGTGC 360
Db 301 CTCACAAAGACAGAGTGTGACAGCAGACATCATGTGTGACAAAGACATGTTCTGTGC 360
QY 361 CTCATGAACACAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGAC 420
Db 361 CTCATGAACACAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGAC 420
QY 421 CCCACGCGCCCACTGTGACAGCAGTGTATGACCGCCCTGTGAGGAGGTGACCTGCAGTACACCA 480
Db 421 CCCACGCGCCCACTGTGACAGCAGTGTATGACCGCCCTGTGAGGAGGTGACCTGCAGTACACCA 480
QY 481 TCCCGAGCGCCCGCCCGCCCTCCCTAG 507
Db 481 TCCCGAGCGCCCGCCCGCCCTCCCTAG 507
RESULT 2
AX304469 AX304469 2270 bp DNA linear PAT 30-NOV-2001
LOCUS Sequence 7 from Patent WO0185956.
DEFINITION

AX304469 AX304469.1 GI:17383840
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Das, D., Reddy, R., Yao, M.G., Nguyen, D.B., Lu, Y., Triboulet, C.M., Yue, H., Khan, F.A., Gandhi, A.R., Au-Young, J., Lal, P., Kearney, L., Elliott, V.S., Ding, L. and Thornton, M.
TITLE Lipid metabolism enzymes
JOURNAL Patent: WO 0185956-A 7 15-NOV-2001;
FEATURES
source location/Qualifiers
1..2270
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 7473224CBL"
BASE COUNT 476 a 690 c 709 g 395 t
ORIGIN
Query Match 100.0%; Score 507; DB 6; Length 2270;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCTTGTGCGCAGCGTTCTGTCCACAGCTCAGCGC 60
Db 222 ATGAAGAAGTTCTTACCGTGGCCATCTTGTGCGCAGCGTTCTGTCCACAGCTCAGCGC 281
QY 61 AGCGTCTCAACTGAAGGCCATGTGAGGCGCGTCACAGGAGGAGCGCCATCTCTGCC 120
Db 282 AGCGTCTCAACTGAAGGCCATGTGAGGCGCGTCACAGGAGGAGCGCCATCTCTGCC 341
QY 121 TTCGTGGGCTACGGTTGCTTACTGTGGGCTGGGGCGCGTCACAGGAGGAGCGCG 180
Db 342 TTCGTGGGCTACGGTTGCTTACTGTGGGCTGGGGCGCGTCACAGGAGGAGCGCG 401
QY 181 GACTGTGTGCGCCACCGCCACGCTGCTGTACAGGAACTCTTTGACCAAGCGCTGTAC 240
Db 402 GACTGTGTGCGCCACCGCCACGCTGCTGTACAGGAACTCTTTGACCAAGCGCTGTAC 461
QY 241 CCTATGTGGACCACTATGATCACCACATCGAGAACACACTGAGATAGTCTGCAGTGAC 300
Db 462 CCTATGTGGACCACTATGATCACCACATCGAGAACACACTGAGATAGTCTGCAGTGAC 521
QY 301 CTCACAAAGACAGAGTGTGACAGCAGACATCATGTGTGACAAAGACATGTTCTGTGC 360
Db 522 CTCACAAAGACAGAGTGTGACAGCAGACATCATGTGTGACAAAGACATGTTCTGTGC 581
QY 361 CTCATGAACACAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGAC 420
Db 582 CTCATGAACACAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGACAGCAGAGTGTGAC 641
QY 421 CCCACGCGCCCACTGTGACAGCAGTGTATGACCGCCCTGTGAGGAGGTGACCTGCAGTACACCA 480
Db 642 CCCACGCGCCCACTGTGACAGCAGTGTATGACCGCCCTGTGAGGAGGTGACCTGCAGTACACCA 701
QY 481 TCCCGAGCGCCCGCCCGCCCTCCCTAG 507
Db 702 TCCCGAGCGCCCGCCCGCCCTCCCTAG 728
RESULT 3
AK093645 AK093645 2716 bp mRNA linear PRI 15-JUL-2002
LOCUS Homo sapiens cDNA FLJ36326 fis, clone THYM2005576, moderately similar to Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA.
DEFINITION
ACCESSION
VERSION AK093645.1 GI:21752561
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens thymus cDNA to mRNA, Clone_lib:THYM02

```

clone:THYMU2005576.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
Arita,M., Mueashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,
Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H.,
Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A.,
Kavakani,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuho,Y., Nagai,K.
and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2716)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
key Technology Center etc.); 5'- & 3'-end one pass sequenced by RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
Location/Qualifiers
1..2716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="THYMU2005576"
/tissue_type="shymus"
/clone_lib="THYMU2"
/notes="cloning vector: pME18SFL3"
232..738
/notes="unnamed protein product"
/codon_start=1
/protein_id="BAC04210.1"
/db_xref="GI:21752562"
/translation="MKKFTVAILAGSVLSTAHGSLNLLKAMVEAVTGRSAILSVFGY
GCYCGIGGGRQPKDEVDWCCHADCCYQELFDGCHPYVDHYDHTIENNTIIVGSDLN
SPAPPAPP"
BASE COUNT 568 a 844 c 838 g 466 t
ORIGIN
Query Match 99.7%; Score 505.4; DB 9; Length 2716;
Best Local Similarity 99.8%; Pred. No. 3.3e-103;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTCTGGCAGGCTTCTGCCACAGCTCACGGC 60
DB 232 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTCTGGCAGGCTTCTGCCACAGCTCACGGC 291
QY 61 AGCTGCTCAACCTGAAGCCATGTTGGAGCGCGTTCACAGGAGGAGCGCCATCCTGTC 120
DB 292 AGCTGCTCAACCTGAAGCCATGTTGGAGCGCGTTCACAGGAGGAGCGCCATCCTGTC 351
QY 121 TTCTGGGCTTACGGTTGCTACTGTGGGCTGGGGCGCGTTCACAGGAGGAGCGCCATCCTGTC 180
DB 352 TTCTGGGCTTACGGTTGCTACTGTGGGCTGGGGCGCGTTCACAGGAGGAGCGCCATCCTGTC 411
QY 181 GACTGTGTGTCACCGCCACGACTGCTCTACCGAGAACTCTTTGACCAAGGCTGTGCAC 240
DB 412 GACTGTGTGTCACCGCCACGACTGCTCTACCGAGAACTCTTTGACCAAGGCTGTGCAC 471
QY 241 CCTATGTGGACCACTATGATCACACCATCGAGAACACACTGAGATAGTCTGCAGTGAC 300
DB 472 CCTATGTGGACCACTATGATCACACCATCGAGAACACACTGAGATAGTCTGCAGTGAC 531

```

```

QY 301 CTCACAAGACAGAGTGTGACAGCAGACATGCATGTGTGACAAAGAACATGTTCTGTGC 360
DB 532 CTCACAAGACAGAGTGTGACAGCAGACATGCATGTGTGACAAAGAACATGTTCTGTGC 591
QY 361 CTCATGAACACAGCTACCGAGAGGAGTACCGTGGCTTCCCTCAATGTCTACTGCCAGGC 420
DB 592 CTCATGAACACAGCTACCGAGAGGAGTACCGTGGCTTCCCTCAATGTCTACTGCCAGGC 651
QY 421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCTGAGGAGGTACCTGCAGTCCACAA 480
DB 652 CCCACGCCCAACTGCAGCATCTATGAACCGCCCTGAGGAGGTACCTGCAGTCCACAA 711
QY 481 TCCCAGCGCCCGCCCGCCCTCCCTAG 507
DB 712 TCCCAGCGCGCCCGCCCGCCCTAG 738
RESULT 4
LOCUS AF166099 906 bp mRNA linear ROD 02-NOV-1999
DEFINITION Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA,
complete cds.
ACCESSION AF166099
VERSION AF166099
KEYWORDS AF166099.2 GI:6174880
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 906)
Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
On the diversity of secreted phospholipases A(2). Cloning, tissue
distribution, and functional expression of two novel mouse group II
enzymes
J. Biol. Chem. 274 (44), 31195-31202 (1999)
JOURNAL 20002639
MEDLINE 10531313
PUBMED
REFERENCE 2 (bases 1 to 906)
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles,
Valbonne 06560, France
REFERENCE 3 (bases 1 to 906)
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1999) IPMC, CNRS, 660, route des Lucioles,
Valbonne 06560, France
REMARK Sequence update by submitter
COMMENT On Nov 2, 1999 this sequence version replaced gi:6164699.
FEATURES
Location/Qualifiers
1..906
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
1..906
/gene="pla2g2f"
251..757
/gene="Pla2g2f"
/EC_number="3.1.1.4"
/notes="Ca2+-dependent secreted phospholipase A2"
/codon_start=1
/product="group IIF secreted phospholipase A2"
/protein_id="AF04500.2"
/db_xref="GI:6174881"
/translation="MKKFFAIVLAGSVVTTAHSLLNLSKMSVEATHRNLSILSVFGY
GCYCGIGGGRHPMDVWCCHADCCYQELFDGCHPYVDHYDHTIENNTIIVCTELN
ETECCKQTCEDCKSLTLCKDHPYRNRYGVNYVYCGPTNCSLYDPYEEVTCGHG
LPATPVST"
BASE COUNT 208 a 265 c 256 g 177 t
ORIGIN
Query Match 67.2%; Score 340.6; DB 10; Length 906;
Best Local Similarity 79.5%; Pred. No. 3.3e-66;

```



```

repeat_region 18810. .18923
/Note="3 copies 38 mer 77% conserved"
repeat_region 20154. .20297
/Note="9 copies 16 mer 72% conserved"
repeat_region 20297. .20340
/Note="22 copies 2 mer tg 81% conserved"
misc_feature 25520. .25869
/Note="match: GSS: Em:AQ225965"
misc_feature 25529. .25754
/Note="match: GSS: Em:B58996"
repeat_region 29107. .29271
/Note="MER45 repeat: matches 1. .178 of consensus"
repeat_region 29272. .29333
/Note="MER45B repeat: matches 975. .1039 of consensus"
repeat_region 30193. .30260
/Note="L1MC/D repeat: matches 5706. .5775 of consensus"
misc_feature complement(31785. .32194)
/Note="match: GSS: Em:AQ277413"
misc_feature 32909. .33153
/Note="match: GSS: Em:B15515"
repeat_region 33499. .33681
/Note="LTR16A repeat: matches 121. .295 of consensus"
repeat_region 33695. .33870
/Note="11 copies 16 mer 64% conserved"
repeat_region 33705. .33894
/Note="5 copies 38 mer 66% conserved"
repeat_region 33712. .33867
/Note="78 copies 2 mer tg 64% conserved"
repeat_region 33998. .34201
/Note="8 copies 38 mer 60% conserved"
repeat_region 33991. .34194
/Note="102 copies 2 mer tg 62% conserved"
repeat_region 33998. .34205
/Note="13 copies 16 mer 66% conserved"
repeat_region 34208. .34321
/Note="57 copies 2 mer tg 69% conserved"
repeat_region 34235. .34330
/Note="6 copies 16 mer 71% conserved"
repeat_region 36684. .37082
/Note="MER7A repeat: matches 1. .346 of consensus"
misc_feature 38387. .38773
/Note="match: STS: Em:HS3432A9"
misc_feature 38387. .38685
/Note="match: STS: Em:Z51469"
repeat_region 38691. .38726
/Note="18 copies 2 mer ca 97% conserved"
misc_feature join(38780. .39119, 40855. .40926)
/Note="match: STS: Em:Aa479352"
misc_feature 40367. .40803
/Note="CpG island"
/Note="evidence-not_experimental"
repeat_region 44473. .44664
/Note="MER58 repeat: matches 1. .198 of consensus"
misc_feature complement(45904. .46320)
/Note="match: STS: Em:AA394141"
misc_feature complement(45950. .46366)
/Note="match: STS: Em:T86344"
misc_feature complement(46154. .46576)
/Note="match: GSS: Em:AQ340310"
misc_feature complement(48597. .49196)
/Note="match: STS: Em:AA135547"
repeat_region 52724. .53004
/Note="L1MC1 repeat: matches 5600. .5876 of consensus"
repeat_region 61040. .61202
/Note="FRAM repeat: matches 2. .162 of consensus"
repeat_region 63305. .63419
/Note="FLAM-C repeat: matches 2. .119 of consensus"
repeat_region 67470. .67491
/Note="11 copies 2 mer aa 100% conserved"
repeat_region 82874. .83099
/Note="LTR16A repeat: matches 214. .443 of consensus"
repeat_region 86860. .87858
/Note="MER11A repeat: matches 1. .1266 of consensus"

```

```

repeat_region 91919. .92837
/Note="MER49 repeat: matches 7. .923 of consensus"
repeat_region 93468. .93679
/Note="MER4B repeat: matches 3. .175 of consensus"
repeat_region 93975. .94012
/Note="MER4B repeat: matches 175. .212 of consensus"
repeat_region 94013. .94077
/Note="MER4D repeat: matches 388. .451 of consensus"
repeat_region 94377. .94937
/Note="MER4D repeat: matches 451. .1015 of consensus"
repeat_region 98792. .98904
/Note="MER81 repeat: matches 1. .114 of consensus"
repeat_region 99914. .100001
/Note="MSTD repeat: matches 313. .394 of consensus"
repeat_region 100002. .100283
/Note="MSTC repeat: matches 1. .317 of consensus"
repeat_region 102743. .103070
/Note="MER41A repeat: matches 1. .328 of consensus"
repeat_region 103071. .103258
/Note="L1PA7 repeat: matches 5960. .6141 of consensus"
repeat_region 103288. .103525
/Note="MER41A repeat: matches 316. .554 of consensus"

Query Match 41.8%; Score 212; DB 9; Length 135571;
Best Local Similarity 100.0%; Pred. No. 1.7e-37;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 GTGACCTCAACAGACAGAGTGTGACAGACAGACATGTCGTGACAGACATGGTTC 355
|||||
Db 2689 GTGACCTCAACAGACAGAGTGTGACAGACAGACATGTCGTGACAGACATGGTTC 2748

Qy 356 TGTGCCTCATGAACACAGACCTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 415
|||||
Db 2749 TGTGCCTCATGAACACAGACCTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 2808

Qy 416 AGGGCCACGCCCCCACTGCAGCATCTATGAACGCGCCCTGAGGAGGTACCTGCAGTTC 475
|||||
Db 2809 AGGGCCACGCCCCCACTGCAGCATCTATGAACGCGCCCTGAGGAGGTACCTGCAGTTC 2868

Qy 476 ACCAATCCCGAGCGCCCGCCCGCCCTCCCTAG 507
|||||
Db 2869 ACCAATCCCGAGCGCCCGCCCGCCCTCCCTAG 2900

RESULT 6
LOCUS
DEFINITION
AL158172
Human DNA sequence from clone Rpl-169023 on chromosome 1 Contains
ESTs, STSs and GSSs. Contains the PLA2G5 gene for two isoforms of
phospholipase A2 group V, a novel gene, the PLA2G2D gene for
phospholipase 2 group IID and the 5' part of the gene for a novel
phospholipase similar to mouse phospholipase A2 group IIF
(PLA2G2F), complete sequence.
ACCESSION
AL158172
VERSION
AL158172.5 GI:9801324
KEYWORDS
HTG: phospholipase; PLA2G2D; PLA2G2F; PLA2G5.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 98743)
AUTHORS
Wallis J.
TITLE
Direct Submission
JOURNAL
Submitted (25-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 14, 2000 this sequence version replaced gi:9714699.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

```

Mon Feb 10 11:35:45 2003

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr1>

RP1-169023 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone

RP1-169023. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP1-169023 is at 1 in this sequence. The true left end of clone RP3-340N1 is at 98644 in this sequence.

FEATURES

source	Location/Qualifiers
misc_feature	1..98743
misc_feature	/organism="Homo sapiens"
misc_feature	/db_xref="taxon:9606"
misc_feature	/chromosome="1"
misc_feature	/clone="RP1-169023"
misc_feature	/clone_lib="RPCI-1"
repeat_region	107..371
repeat_region	/note="match: GSS: Em:B75013"
repeat_region	complement(249..658)
repeat_region	/note="match: STS: Em:G50772"
repeat_region	match: GSS: Em:AQ201252"
repeat_region	630..756
repeat_region	/note="MER83-internal repeat: matches 1668..1825 of consensus"
repeat_region	781..909
repeat_region	/note="MER65-internal repeat: matches 1665..1801 of consensus"
repeat_region	928..1655
repeat_region	/note="MER4-internal repeat: matches 1764..2472 of consensus"
repeat_region	1636..1896
repeat_region	/note="LTR8 repeat: matches 1..257 of consensus"
repeat_region	1897..2592
repeat_region	/note="MER4-internal repeat: matches 2472..3484 of consensus"
repeat_region	2593..2950
repeat_region	/note="THE1B repeat: matches 1..364 of consensus"
repeat_region	2951..3152
repeat_region	/note="MER4-internal repeat: matches 3484..3679 of consensus"
repeat_region	3157..5261
repeat_region	/note="MER4-internal repeat: matches 3840..6087 of consensus"
repeat_region	5262..5337
repeat_region	/note="AluI repeat: matches 228..303 of consensus"
repeat_region	5338..5858
repeat_region	/note="MER4-internal repeat: matches 6087..6596 of consensus"
repeat_region	5866..6336
repeat_region	/note="MER42 repeat: matches 1..504 of consensus"
repeat_region	6337..6694
repeat_region	/note="L1MC4 repeat: matches 6189..6548 of consensus"
repeat_region	6897..7044
repeat_region	/note="L1MC2 repeat: matches 6050..6202 of consensus"
repeat_region	7063..7122
repeat_region	/note="MLTIE repeat: matches 507..567 of consensus"
repeat_region	7800..8099
repeat_region	/note="L1M4 repeat: matches 5497..5798 of consensus"
misc_feature	complement(7990..8417)
misc_feature	/note="match: GSS: Em:AQ263839"
misc_feature	complement(8044..8537)
misc_feature	/note="match: GSS: Em:AQ591805"
repeat_region	8198..8361
repeat_region	/note="L2 repeat: matches 2537..2705 of consensus"
repeat_region	8984..9131
repeat_region	/note="L2 repeat: matches 2414..2576 of consensus"
repeat_region	9244..9359
repeat_region	/note="L1MC1 repeat: matches 6210..6327 of consensus"
repeat_region	9376..9483
repeat_region	/note="L1PAL3 repeat: matches 651..544 of consensus"
repeat_region	9520..10539
repeat_region	/note="L1M4 repeat: matches 2963..3988 of consensus"
repeat_region	10553..10664
repeat_region	/note="L1M4 repeat: matches 2243..2357 of consensus"
repeat_region	10655..10936
repeat_region	/note="AluSx repeat: matches 5..276 of consensus"
repeat_region	10937..10951
repeat_region	/note="L1M4 repeat: matches 2230..2244 of consensus"
repeat_region	10939..11702
repeat_region	/note="L1MEC repeat: matches 2206..2980 of consensus"
repeat_region	12233..12282
repeat_region	/note="AluSx repeat: matches 251..302 of consensus"
repeat_region	12293..12588
repeat_region	/note="AluJo repeat: matches 1..306 of consensus"
repeat_region	join(12774..12834,16626..16744,22015..22080,44003..44308)
repeat_region	/gene="dJ169023.2"
repeat_region	join(<12774..12834,16626..16744,22015..22080,44003..44308)
repeat_region	/gene="dJ169023.2"
repeat_region	/product="dJ169023.2.1 (novel protein)"
repeat_region	/note="match: ESTs: Em:AA402475 Em:AA293827"
repeat_region	/evidence=not_experimental
repeat_region	13384..13694
repeat_region	/note="AluSx repeat: matches 1..312 of consensus"
repeat_region	13868..14158
repeat_region	/note="AluSp repeat: matches 1..309 of consensus"
repeat_region	14447..14752
repeat_region	/note="AluJb repeat: matches 3..307 of consensus"
repeat_region	15010..15387
repeat_region	/note="MSTA repeat: matches 1..426 of consensus"
repeat_region	15654..15790
repeat_region	/note="AluJo repeat: matches 1..133 of consensus"
repeat_region	16192..16348
repeat_region	/note="AluJo repeat: matches 137..296 of consensus"
repeat_region	join(16736..16744,22015..22080,44003..44032)
repeat_region	/gene="dJ169023.2"
repeat_region	/note="5' UTR probably continues in BA66M4 (AL360079)
repeat_region	3rd exon misses correct 3' splice site"
repeat_region	/codon_start=1
repeat_region	/evidence=not_experimental
repeat_region	/product="dJ169023.2.1 (novel protein)"
repeat_region	/protein_id="CAC13157.1"
repeat_region	/db_xref="GI:10862734"
repeat_region	/translation="MSMPLIQPEGTHSPRPTQQSQESDSGHRTW"
repeat_region	17434..17743
repeat_region	/note="AluSx repeat: matches 1..309 of consensus"
repeat_region	17754..17885
repeat_region	/note="F1AM_C repeat: matches 1..132 of consensus"
repeat_region	complement(17768..18077)
repeat_region	/note="match: GSS: Em:AQ880240"
repeat_region	17957..18057
repeat_region	/note="MER5A repeat: matches 10..109 of consensus"
repeat_region	18254..18995
repeat_region	/note="L1MC2 repeat: matches 5582..6328 of consensus"
repeat_region	19004..19128
repeat_region	/note="FAM repeat: matches 1..124 of consensus"
repeat_region	19139..19511
repeat_region	/note="L1MC2 repeat: matches 5204..5592 of consensus"
repeat_region	19567..19724
repeat_region	/note="MER63 repeat: matches 1..783 of consensus"
repeat_region	19867..20140
repeat_region	/note="AluJo repeat: matches 1..265 of consensus"


```

misc_feature      88339..107178
/note="assembly_fragment:00095
fragment_chain:2"
misc_feature      107279..159991
/note="assembly_fragment:00877
fragment_chain:2"
misc_feature      160092..175174
/note="assembly_fragment:01936
fragment_chain:2"
misc_feature      175275..186589
/note="assembly_fragment:00819
fragment_chain:2
clone_end:SP6
vector_side:right"
BASE COUNT      47647 a 45898 c 45957 g 45956 t 1131 others
ORIGIN

Query Match      26.8%; Score 135.8; DB 2; Length 186589;
Best Local Similarity 77.7%; Pred. No. 2.1e-20;
Matches 164; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 297 TGACCTCAACAAGACAGAGAGTGTGACAAAGCAGACATGTCGACAAAGACATGTTCT 356
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51156 TGAGCTCAATGAGCGAGTGTGACAAAGCAGACATGTCGACAAAGCCTGACTCT 51097
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 357 GTGCCTCATGACACAGCTACCGAGAGGATACCGTGGCTTCTCAATGTTACTGCCA 416
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51096 GTGCCTCAAGATACCCATCAGGAGAAAGTACCGAGGCTACTTCAACGTCTACTGCCA 51037
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 417 GGGCCCCACGCCCACTGACGATCTATGAACGCCGCCCTGAGAGGATCACTGCGAGTCA 476
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51036 GGGCCCCACACCCCACTGACGATCTATGACCGTGATACCCAGAGAGTCACTGTTGGCA 50977
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 477 CCAATGCCAGCGCCCGCCCGCCCTCCTAG 507
||||| ||||| ||||| ||||| |||||
Db 50976 TGGGCTCCTCGACCGCCCTGCTCAACCTAG 50946
||||| ||||| ||||| ||||| |||||

RESULT 8
AC118094
LOCUS      Rattus norvegicus clone CH230-117D17, *** SEQUENCING IN PROGRESS
DEFINITION *** 74 unordered pieces.
ACCESSION AC118094
VERSION    AC118094.4 GI:21746730
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 157317)
            Muzny D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
            Alsbrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,
            Barbria, J., Benton, J., Bmaga, K., Blankenburg, K., Bonnin, D.,
            Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
            Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
            Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
            Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
            Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
            Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
            Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
            Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
            Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
            Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
            Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
            Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
            Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
            Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
            Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
            Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
            Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
            Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
            Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H.,
            Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
            Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
            Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
            Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
            Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
            Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
            Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
            Peters, L., Pickens, R., Primus, E., Pu, L.L., Ruiz, S., Savary, G.,
            Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
            Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
            Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H.,
            Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
            Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
            Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
            Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
            Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
            Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
            Weinstein, G. and Gibbs, R.
            Submitted (13-APR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 157317)
            Worley, K.C.
            Direct Submission
            Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Jul 14, 2002 this sequence version replaced gi:20258206.
            ----- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ----- Project Information
            Center project name: GUXU
            Center clone name: CH230-117D17
            ----- Summary Statistics
            Sequencing vector: Plasmid;
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990329
            Consensus quality: 98821 bases at least Q40
            Consensus quality: 107462 bases at least Q30
            Consensus quality: 113497 bases at least Q20
            -----
            * NOTE: Estimated insert size may differ from sequence length
            * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 74 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N. But the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1464: contig of 1464 bp in length
            * 1465: gap of unknown length
            * 1565: contig of 1165 bp in length
            * 2730: gap of unknown length
            * 2829: gap of unknown length
            * 4337: contig of 1508 bp in length
            * 4338: gap of unknown length
            * 4437: gap of unknown length
            * 5750: contig of 1313 bp in length
            * 5850: gap of unknown length
            * 5951: contig of 1085 bp in length
            * 6936: gap of unknown length
            * 7036: contig of 1785 bp in length
            * 8821: gap of unknown length
            * 8921: contig of 1080 bp in length

```


Mon Feb 10 11:35:45 2003

```

Hernandez,O., Hodson,A., Hognes,M., Holloway,C., Hollins,B.,
Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Noguer,M., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaiké,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 176574)
Worley,K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 176574)
Worley,K.C.
Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:18138623.
-----
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----
Project Information
Center project name: GHKJ
Center clone name: CH230-14317
-----
Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 121890 bases at least Q40
Consensus quality: 126967 bases at least Q30
Consensus quality: 131259 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1559: contig of 1559 bp in length
* 1560 1659: gap of unknown length
* 1660 2681: contig of 1022 bp in length
* 2682 2781: gap of unknown length
* 2782 3838: contig of 1057 bp in length
* 3839 3938: gap of unknown length
* 3939 5116: contig of 1178 bp in length
* 5117 5216: gap of unknown length
6337: contig of 1121 bp in length
6437: gap of unknown length
7507: contig of 1070 bp in length
7607: gap of unknown length
9007: contig of 1400 bp in length
9107: gap of unknown length
10354: contig of 1247 bp in length
10455 11521: contig of 1067 bp in length
11621: gap of unknown length
12787: contig of 1166 bp in length
12887: gap of unknown length
14400: contig of 1513 bp in length
14500: gap of unknown length
15587: contig of 1087 bp in length
15687: gap of unknown length
16713: contig of 1026 bp in length
16813: gap of unknown length
18363: contig of 1550 bp in length
18463: gap of unknown length
19680: contig of 1217 bp in length
19780: gap of unknown length
21131: contig of 1351 bp in length
21231: gap of unknown length
22766: contig of 1335 bp in length
22866: gap of unknown length
24218: contig of 1352 bp in length
24318: gap of unknown length
25650: contig of 1332 bp in length
25750: gap of unknown length
27009: contig of 1259 bp in length
27109: gap of unknown length
28612: contig of 1503 bp in length
28712: gap of unknown length
30102: contig of 1390 bp in length
30202: gap of unknown length
32258: contig of 2056 bp in length
32358: gap of unknown length
34204: contig of 1846 bp in length
34304: gap of unknown length
35879: contig of 1575 bp in length
35979: gap of unknown length
37987: contig of 2008 bp in length
38087: gap of unknown length
40417: contig of 2330 bp in length
40517: gap of unknown length
42940: contig of 2423 bp in length
43040: gap of unknown length
45079: contig of 2039 bp in length
45179: gap of unknown length
46971: contig of 1792 bp in length
47071: gap of unknown length
48516: contig of 1445 bp in length
48616: gap of unknown length
49920: contig of 1304 bp in length
50020: gap of unknown length
51973: contig of 1953 bp in length
52073: gap of unknown length
53823: gap of unknown length
55124: contig of 1301 bp in length
55224: gap of unknown length
57631: contig of 2407 bp in length
57731: gap of unknown length
60252: contig of 2521 bp in length
60352: gap of unknown length
62016: contig of 1664 bp in length
62116: gap of unknown length
64838: contig of 2722 bp in length
64938: gap of unknown length
66738: contig of 1798 bp in length
66838: gap of unknown length
69879: contig of 3043 bp in length

```

FEATURES		Location/Qualifiers	
source	1. .878	/organism="Homo sapiens"	
gene	1. .878	/db_xref="taxon:9606"	
CDS	29. .466	/gene="PLA2"	
		/gene="PLA2"	
		/note="group IID SPLA2"	
		/codon_start=1	
		/product="group IID secretory phospholipase A2"	
		/protein_id="AAD51390.1"	
		/db_xref="GI:5771420"	
variation	GCHGLGSGQPKDATDWCCQTHDCQYDLKTCGCGIYKDYRYNFSQGNHICSDKGS WCQQQLCACDKEVAFCLRNLDYQRLRYWPHRCGTGPGC"		
	266		
	/gene="PLA2"		
	/note="results in glycine to serine substitution"		
	/replace="a"		
BASE COUNT	206 a	257 c	238 g 177 t
ORIGIN			
Query Match	19.5%;	Score 99;	DB 9; Length 878;
Best Local Similarity	57.2%;	Pred. No. 5.1e-12;	
Matches 202;	Conservative 0;	Mismatches 145;	Indels 6; Gaps 1;
QY	40	GTCTCTGCACAGCTCACGGCAGCTCTCAACCTGAAGCCATGGTGGAGCGCTCAC	99
Db	68	GGTGTATTCCAAATCCAGGGCGGGATCTCTCAACCTGAAGATGGTCAAGCAAGTCACT	127
QY	100	GGGAGGAGCCCATCTCTCTTCTGGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGT	159
Db	128	GGGAAATGGCCATCT	187
QY	160	GGCCAGCCCAAGGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	219
Db	188	GGCCAAACCAAGATGCCAGGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	247
QY	220	CTCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCACTCGAGAACA	279
Db	248	CTGAAGACCCAGGGTGGCGCATCTACAGGACTATTACAGATACAACTT-----TTCC	301
QY	280	ACTGAGATAGTCTGCAGTGCACCTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGT	339
Db	302	CAGGGACATCCACTGCTCTGACAAGGAGTGGTGTGTGAGCAGCAGCTGTGTGCTGTGT	361
QY	340	GACAAGAACATGGTGTGTGCTCATGAACCAAGACCTACCGAGAGGAGTACCG	392
Db	362	GACAAGAGGTGGCTTCTGCTCTGAAGCGCAACCTGCACACCTACCGAAGCG	414
RESULT 11			
AF188625			
LOCUS	AF188625	1938 bp	mrna linear PRI 28-AUG-2000
DEFINITION	Homo sapiens phospholipase A2 (SPLASH) mRNA, complete cds.		
ACCESSION	AF188625		
VERSION	AF188625.1	GI:6453792	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1938)		
TITLE	Shakhov.A.N., Rubtsov.A.V., Lyakhov,I.G., Tumanov.A.V. and Nedospasov,S.A.		
JOURNAL	SPLASH (PLA2IID), a novel member of phospholipase A2 family, is associated with lymphotoxin deficiency		
MEDLINE	Genes Immun. 1 (3), 191-199 (2000)		
PUBMED	21040292		
REFERENCE	11196711		
AUTHORS	2 (bases 1 to 1938)		
	Shakhov.A.N., Rubtsov.A.V., Lyakhov,I.G., Tumanov.A.V. and		

* 69880		59979: gap of unknown length	
* 72698		contig of 2719 bp in length	
* 72599		gap of unknown length	
* 72799		contig of 1982 bp in length	
* 74781		gap of unknown length	
* 74881		contig of 2465 bp in length	
* 77346		gap of unknown length	
* 77446		contig of 2847 bp in length	
* 80293		gap of unknown length	
* 80393		contig of 3175 bp in length	
* 83568		gap of unknown length	
* 83668		contig of 2945 bp in length	
* 86613		gap of unknown length	
* 86713		contig of 2141 bp in length	
* 88854		gap of unknown length	
* 88954		contig of 2778 bp in length	
* 91732		gap of unknown length	
* 91831		contig of 3783 bp in length	
* 95615		gap of unknown length	
* 95715		contig of 3573 bp in length	
* 99288		gap of unknown length	
* 99388		contig of 2561 bp in length	
* 101949		gap of unknown length	
* 102049		contig of 3778 bp in length	
* 105827		gap of unknown length	
* 105927		contig of 3434 bp in length	
Query Match		25.5%; Score 129.4; DB 2: Length 176574;	
Best Local Similarity		75.8%; Pred. No. 5.7e-19;	
Matches 160;		Conservative 0;	Mismatches 51; Indels 0; Gaps 0;
QY	297	TGACCTCAACAGACAGATGTGACAAGCAGACATGCTATGTGTGACAAGACATGGTTCT	356
Db	167689	TGAGCTCAATGAGACCGCGTGTGATAAGCAGCGTGTGACTGTGACAAGACCTGACTCT	167630
QY	357	GTGCCTCATGAACGACGCTACCGAGAGTACCGTGGCTTCTCTCAATGTCTACTGCCA	416
Db	167629	GTGCCTCAAGGACCATCGTACAGGAAAGTACCAGGCGTACCTCAATGTCTACTGTCA	167570
QY	417	GGGCCCCACGCCCACTGCAGCATCTATGAACCGCCCTGAGGAGGTCACTCACTGCTCA	476
Db	167569	CGSCCCACACCCAACTGCAGCATCTACGACCGTACCAGGAGTCACTCTGTGACA	167510
QY	477	CCAATCCCGAGCGCCCGCCCTCCCTAG	507
Db	167509	TGCGCTCTCAACAACCCGTGTCTCAACCTAG	167479
RESULT 10			
AF112982			
LOCUS	AF112982	878 bp	mrna linear PRI 30-AUG-1999
DEFINITION	Homo sapiens group IID secretory phospholipase A2 (PLA2) mRNA, complete cds.		
ACCESSION	AF112982		
VERSION	AF112982.1	GI:5771419	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 878)		
TITLE	Ishizaki,J., Suzuki,N., Higashino,K., Yokota,Y., Ono,T., Kawamoto,K., Fujii,N., Arita,H. and Hanasaki,K.		
JOURNAL	Cloning and characterization of novel mouse and human secretory phospholipase A(2)s		
MEDLINE	J. Biol. Chem. 274 (35), 24973-24979 (1999)		
PUBMED	99386983		
REFERENCE	10455175		
AUTHORS	2 (bases 1 to 878)		
TITLE	Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.		
JOURNAL	Direct Submission		
MEDLINE	Submitted (11-DEC-1998) Shionogi Research Laboratories, Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002 Japan		
PUBMED			

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 49 Row: m Column: 9
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA1: 6912595.

```

FEATURES
source
Location/Qualifiers
1. .2747
/organism="Homo sapiens"
/db_xref="LocusID:26279"
/db_xref="taxon:9606"
/clone="MGC:34386 IMAGE:5223912"
/tissue_type="Pancreas, Spleen, adult pooled"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
18. .455
/codon_start=1
/product="Phospholipase A2, group IID"
/protein_id="AAH25706.1"
/db_xref="GI:19344001"
/translation="METALLICGLVVMAGVPIOGGILNLNKMVKQVTKGKPIILSYWY
WCGQQLGAGQPKADDTWCCTDHCQYDHLKTKGCSLYIKDYIRYFNFSQGNLHCSDKGS
WCQCGLCACDKAEVAFCLKRLDLYQKRLRYWPRHCRGQTGGC"
BASE COUNT
719 a 762 c 668 g 598 t
ORIGIN

```

Query Match	19.5%;	Score 99;	DB 9;	Length 2747;	
Best Local Similarity	57.2%;	Pred. No. 4.8e-12;			
Matches 202;	Conservative 0;	Mismatches 145;	Indels 6;	Gaps 1;	
Qy	40	GTTCGTCCAGCTC	ACGGCAGCCTGCTCAACCTGAAGGCCATGCTGGAGGCCGCTCACA	99	
Db	57	GGTGTGATTC	CAATCCAGGGGGGATCCTGACCTTGAACAGATGGTCAAGCAAGTGACT	116	
Qy	100	GGGAGGAGCGGCATCCTCTTCCTTCGTGGGGCTACGGTTGCTACTGTGGCTGGGGGGCCGT	159		
Db	117	GGGAAATGCCCATCTCTCTACTTGGCCCTACGGCTGTCACTGCGGACTAGTGGCAGA	176		
Qy	160	GGCCAGCCCAAGGATGAGGTGACTGTGTGTCGCCACGCCCCAGCACTGCTGTACCAGNA	219		
Db	177	GGCCAAACCAAGATGCCACGACTGGTGTGCCACAGCCCATGACTGTGCTATGACCAC	236		
Qy	220	CTCTTTGACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCACATCGAGAACAAC	279		
Db	237	CTGAAGACCCAGGGGTGCAGCATCTACAAAGGACTATTACAGATACACTT-----TTCC	290		
Qy	280	ACTGAGATAGTCTGCAGTGACCTCAACAGACAGAGTGTGCAACAGACAGCATGCAATGTT	339		
Db	291	CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGACGACAGCTGTGTGCCCTG	350		
Qy	340	GACAACAACATGGTTCTGTGCCCTATGAACACAGAGCTACCCGAGAGGAGTACCG	392		
Db	351	GACAAGGAGTGGCCCTTGTGCTGAAGGCGCAACCTTGGACACCTACCCAGAAAGCG	403		

```
RESULT 13
AX464400
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L., and Zhang, Z.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL
Patent: WO 0140466-A 533 07-JUN-2001;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
1..496
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT
200 a 95 c 104 g 95 t 2 others
ORIGIN
Query Match 18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 3.1e-11;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 40 GTTCTGCCAGCTCAGCGCGCTCAACCTGAAGCCCATGTGGAGCGCGTCACA 99
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 GGTGTGATTCATCCAGGCGGGATCCTGAACCTGAACAGATGTTCAAGCAAGTGA 127
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 100 GGGAGGAGCGCCATCTCTCGTGGCTAGCGTTGCTACTGTGGCTGGGGGGCGGT 159
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 GGGAAATGCCATCTCTCTACTGGCCCTACGGCTGCTACCTGGGACTAGTGGCAGA 187
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 160 GCGCAGCCCAAGTAGAGTGGACTGTGTGCGACGCCACACACTGCTGTACCAAGGAA 219
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 GGCAACCCCAAGATGCCAGGACTGTGTGCGACGCCACCTGCTGTCTATGACCAC 247
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 220 CTCTTTGCCAAGGCTGTACCCCTATGTGACCACTATATCATCACCAT 269
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 CTGAAGACCCAGGGTGGCGCATCTACAAGGACAACAAAGACGACAT 297
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
MMU18119
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1445)
REFERENCE
AUTHORS
Balboa, M.A., Balsinde, J., Winstead, M.V., Tischfield, J.A. and
Dennis, E.A.
TITLE
Novel group V phospholipase A2 involved in arachidonic acid
mobilization in murine P388D1 macrophages
J. Biol. Chem. 271 (50), 32381-32384 (1996)
97113049
MEDLINE
PUBMED
8943302
REFERENCE
AUTHORS
Chen, J., Shao, C., Lazar, V., Srivastava, C.H., Lee, W.H. and
Tischfield, J.A.
TITLE
Localization of group IIC low molecular weight phospholipase A2
```

```
mrna to meiotic cells in the mouse
J. Cell. Biochem. 64 (3), 369-375 (1997)
97209919
PUBMED
9057094
REFERENCE
3 (bases 1 to 1445)
AUTHORS
Tischfield, J.A.
TITLE
Direct Submission
JOURNAL
Submitted (05-DEC-1994) Jay A. Tischfield, Medical and Molecular
Genetics, Indiana University School of Medicine, 975 W. Walnut,
Indianapolis, IN 46202, USA
FEATURES
source
Location/Qualifiers
1..1445
/organism="Mus musculus"
/db_xref="taxon:10090"
179..631
/codon_start=1
/evidence=experimental
/product="phospholipase A2"
/protein_id="AAC52936.1"
/db_xref="GI:1049008"
/translation="MKGTAFILFVFTTSLSFHQFQRMVHKVHVTGRSAFFSYGY
GCYGLGKGLUPVDATDRCCWAHDCCHLKKEYGCPILNAYQFTIYVNGTIVTCGCTVA
SSCPGQKACEDKQSVYCFKENLATVEKAFKQLFTRPQCGDRKLOC"
BASE COUNT
361 a 388 c 384 g 312 t
ORIGIN
Query Match 18.4%; Score 93.2; DB 10; Length 1445;
Best Local Similarity 56.4%; Pred. No. 1e-10;
Matches 195; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
QY 47 CCACAGCTCAGCGCAGCTGCTCAACCTGAAGCCCATGTGGAGCGCGTCACAGGAGGA 106
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 CTTCCACCTCAGCAGATTTCTGGCAGTTCACAGAGATGTCAACACGTTCACAGGGCGCA 284
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 GGGCCATCTGCTTCCTTCGTGGCTACGGTTGCTACTGTGGCTGGGGGGCCGTGGCCAGC 166
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 GCGCTTCTCTCTTATACGGATATGGCTGCTACTGTGGCTTGGGGCAAGGGCTCC 344
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 167 CCAAGGATAGGTGAGTGGTCTGCCAGCCGACGACTGCTGCCAGGAACTCTTTG 226
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 CTGTGGATGCCACAGACAGAGTGTCTGTGGCTCATGCTGTACCAAGCTTAAGG 404
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 227 ACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCATCGAAGAACACTGAGA 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 ATATGGCTGCCAACCCATCTTGAATGCTACCACTTCACTATGATGGAGCGTGA 464
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 287 ---TAGTCTGCAGTGACCTCAACAGACAGAGTGTGACAAGCAGACATGTCATGTGTGACA 343
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 CCGTGGATGCCACCGTGGCAGCAGCTGCCCTGGGGCAGAAAGGCTGTGAGTGTGACA 524
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 344 AGAACATGTTCTGTGCCTCATGAACACGACGTACCGAGAGGAGTA 389
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 AACAGTCTGTACTGCTTCAAGGAGAACCTGGCCACCTACGAGAA 570
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
BC029347
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1480)
REFERENCE
AUTHORS
Strausberg, R.
TITLE
Direct Submission
JOURNAL
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
1480 bp mrna linear ROD 07-AUG-2002
Mus musculus, Similar to phospholipase A2, group IIC, clone
MGC:18412 IMAGE:4234596, mRNA, complete cds.
BC029347
MGC:18412
BC029347.1
GI:20810357
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 00:07:54 : Search time 227 Seconds
(without alignments)
5029.794 Million cell updates/sec

Title: US-09-975-456B-1

Perfect score: 507

Sequence: 1 atgaagaagtcttcacagt.....cgccccgcgcctccctag 507

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*
1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	100.0	2270	24	ABA96002 Human lipid metabo
2	99	19.5	592	21	AAA53269 Human phospholipas
3	99	19.5	854	22	AAS14884 Human CDNA encodin
4	99	19.5	878	21	AAA60878 Human secretory ph
5	99	19.5	1927	22	AH98759 Human EST-derived
6	99	19.5	1927	22	AAD99768 Human protein enco
7	99	19.5	1931	22	AAD19218 Human CG95 (or C87
8	95.6	18.9	496	21	AAA77684 Human PRO1561 cDNA
9	95.6	18.9	496	22	AAS21510 Human CDNA sequenc

10	95.6	18.9	496	22	AAF54466	DNA encoding prote
11	95.6	18.9	497	21	AAA37132	Human PRO1561 (UNQ
12	86.4	17.0	4325	16	AAQ81136	RPLA2-8 gene. Ra
13	82.8	16.3	1828	16	AAQ81137	RPLA2-10 gene. Ra
14	82.4	16.3	1233	21	AAA72076	cDNA encoding mous
15	82.4	16.3	1233	21	AAA60866	Mouse secretory ph
16	82	16.2	501	21	AAA72077	cDNA fragment enco
17	82	16.2	501	21	AAA60854	Mouse secretory ph
18	76.8	15.1	1014	16	AAQ81138	HPLA2-10 gene. Ho
19	76.8	15.1	1016	24	ABL59517	Human phospholipas
20	75.8	15.0	465	24	ABL58672	Human X-type secre
21	75.8	15.0	465	24	ABA96622	Human X-type secre
22	75.8	15.0	742	20	AA79001	Human phospholipas
23	75.8	15.0	1020	24	ABL58671	Human secretory ph
24	75.8	15.0	1020	24	ABA96621	Human X-type secre
25	75.8	15.0	1737	23	AA591740	DNA encoding novel
26	76.2	14.0	487	22	AA77401	Human phospholipas
27	68.2	13.5	1276	23	AA587642	DNA encoding novel
c	65.8	13.0	445	24	ABL61868	Colon adenocarcino
c	65.8	13.0	445	24	ABL67612	Oesophagus cancer
30	63.8	12.6	1040	24	ABL58680	Mouse X-type secre
31	63.8	12.6	1040	24	ABA96630	Mouse X-type secre
32	61.8	12.2	459	22	AAH42606	Nucleotide sequenc
33	60.8	12.0	518	10	AA91256	DNA sequence of hu
34	60.4	11.9	883	21	AA73130	Mouse secretory ty
35	60.4	11.9	883	22	AA77387	Murine CDNA encodi
36	59.4	11.7	432	14	AAQ48537	Phospholipase A2 c
37	59.4	11.7	470	14	AAQ48538	Phospholipase A2 c
38	57.8	11.4	479	13	AAQ26372	PLA2 CDNA. Synthe
39	57.8	11.4	854	10	AA91258	Nucleotide sequenc
40	57.8	11.4	854	24	ABL69731	Prostate cancer re
41	57.8	11.4	1076	21	AAF15635	Human prostate can
42	57.8	11.4	1116	20	AAZ41274	Human normal ovari
43	57.4	11.3	456	24	ABL60543	Human lipid metabo
44	57.2	11.3	447	24	ABK47377	Human Phospholipas
45	57.2	11.3	562	21	AAF21222	Human low adenosin

ALIGNMENTS

RESULT 1

ABA96002

ID ABA96002 standard; cDNA; 2270 BP.

XX ABA96002;

AC ABA96002;

DT 04-MAR-2002 (first entry)

XX Human lipid metabolism enzyme-2 (LME-2) CDNA.

DE Human; LME-2; lipid metabolism enzyme-2; cytostatic; neuroprotective; immunosuppressive; anti-inflammatory; cardiovascular; gene therapy; enzyme therapy; cancer; neurological disorder; autoimmune disorder; inflammatory disorder; cardiovascular disorder; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 93..728

FT FT /*tag= a

FT FT /product= "LME-2"

XX WO200185956-A2.

PN 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US15210.

XX 11-MAY-2000; 2000US-203511P.

PR 25-MAY-2000; 2000US-207903P.

PR 07-JUN-2000; 2000US-210150P.

PR 23-JUN-2000; 2000US-213392P.

2D NO.7

CC polycystic ovary syndrome, ectopic pregnancies, disruptions of
CC spermatogenesis, cancers within the reproductive tract and impotence.
CC This coding sequence was obtained from clone no.2641779, which was
CC constructed using lung tumour tissue.

XX
SQ Sequence 592 BP; 126 A; 182 C; 165 G; 119 T; 0 other;

Query Match 19.5%; Score 99; DB 21; Length 592;
Best Local Similarity 57.2%; Pred. No. 1.3e-15;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCCACAGCTCAGCGAGCCTGCTCAACCTGAAGGCCATGGTGGAGCCGCTCACA 99
DB 68 GGTGTGATTCACATCCAGGCGGGTCTTGAACCTGAACAGATGGTCAAGCAAGTACT 127
QY 100 GGGAGAGCGCCATCCTGCTTCCTGGGCTACGTTGCTACTGTGGCTGGGGGGCGGT 159
DB 128 GGGAAATGCCCATCTCTCTCTACTGGCCCTACGGCTGTCACTGGCGACTAGGTGGCAGA 187
QY 160 GCCACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
DB 188 GGGCAACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 247
QY 220 CTCCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAC 279
DB 248 CTCAGAGCCCGGGTGGCGGATCTACAAGGACTATTACAGATACAACTT-----TTCC 301
QY 280 ACTGAGATAGTGTGAGTGCCTCAACAGACAGAGTGTGACAGACATGACATGTGT 339
DB 302 CAGGGGAACATCACTGCTCTGACAAAGGAAGTGTGTGAGCAGAGTGTGTGCTGTGT 361
QY 340 GACAGAAATGTTCTGTGCTCTATGACACAGAGCTACCGAGAGAGTACCG 392
DB 362 GACAGGAGGTGGCTCTGCTGCTGAAGCGCAACCTGGACACATACCAAGAGCG 414

RESULT 3

AAS14884

ID AAS14884 standard; cDNA; 854 BP.

AC AAS14884;

DT 20-DEC-2001 (first entry)

DE Human cDNA encoding novel human protein NHP #5.

XX Human; novel human protein; NHP; ss; antidiabetic; antirheumatic;
KW antiarthritic; cystostatic; antiarteriosclerotic; vulnery;
KW neuroprotective; nootropic; antiparkinsonian;
KW anti-human immunodeficiency virus; antisthmatic; vasotrophic; cardiant;
KW hypotensive; anorectic; antifertility; neuroleptic; anticonvulsant;
KW antianemic; immunosuppressive; cerebroprotective; antimicrobial;
KW antiinflammatory; antiseborrheic; antipsoriatic; thyromimetic;
KW immunomodulator; antileishmanial; dermatological; vasoconstriction;
KW gastrointestinal disorder; cardiovascular disorder; hypertension;
KW coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
KW cachexia; male infertility; impotence; testicular cancer; lung tumour;
KW hyperproliferative disorder; pulmonary system disorder;
KW central nervous system disorder; bone disorder;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; schizophrenia; mania; dementia; paranoia;
KW panic disorder; learning disability; amvotropic lateral sclerosis;
KW psychosis; autism; sleep disorder; immune system disorder;
KW Hashimoto's thyroiditis; musculo-skeletal system disorders;
KW multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
KW diabetes mellitus; immunological disorder; asthma; AIDS;
KW acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
KW inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
KW neural system disorder; respiratory disorder; olfactory disorder;
wound healing.

OS Homo sapiens.

XX

PH Key Location/Qualifiers
FT CDS 22..459
FT /*tag= a
FT /product= "NHP #5"
XX
XX WO200174896-A1.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001: 2001WO-US10542.
XX
XX 03-APR-2000: 2000US-194118P.
XX
XX 29-SEP-2000: 2000US-236384P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Moore PA, NI J, Soppet DR, Coleman TA, Gentz RL, Endress GA;
XX
XX Li Y, Dillon PJ;
XX
XX WPI: 2001-626394/72.
XX
XX P-PSDB: AAU09096.
XX
XX New human proteins, useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cardiovascular
XX disorders, autoimmune disorders and reproductive disorders -
XX
XX Claim 1: Page 294; 318pp; English.

XX The invention relates to novel human proteins (NHP) and the
XX nucleic acids that encode them and antibodies raised against them.
XX The proteins, antibodies and nucleic acids are useful in the diagnosis,
XX prognosis, prevention and/or treatment of diseases and/or disorders
XX involving vasoconstriction, gastrointestinal disorders, cardiovascular
XX disorders (e.g. hypertension, erectile dysfunction, high blood pressure,
XX coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,
XX cachexia, disorders of small intestine, disorders of reproductive system
XX (e.g. male infertility and/or impotence), testicular cancer, lung tumours
XX and other hyperproliferative disorders, disorders of pulmonary system,
XX central nervous system disorders, bone disorders, neurodegenerative
XX diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
XX disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
XX panic disorder, learning disabilities, amvotropic lateral sclerosis,
XX psychoses, autism, sleep disorders), immune system disorders (e.g.
XX Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
XX central nervous system disorders (e.g. multiple sclerosis, ischaemic
XX brain injury and/or stroke), infectious diseases, diabetes mellitus,
XX immunological disorders (e.g. asthma, acquired immunodeficient syndrome
XX (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
XX sepsis, acne, psoriasis and lupus erythematosus), neural system
XX disorders, respiratory disorders, olfactory disorders and wound
XX healing. The present sequence encodes an NHP of the invention.

XX
SQ Sequence 854 BP; 186 A; 254 C; 238 G; 176 T; 0 other;

Query Match 19.5%; Score 99; DB 22; Length 854;
Best Local Similarity 57.2%; Pred. No. 1.4e-15;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;

QY 40 GTTCTGTCCACAGCTCAGCGAGCCTGCTCAACCTGAAGGCCATGGTGGAGCCGCTCACA 99
DB 61 GGTGTGATTCACATCCAGGCGGGTCTCTGAACCTGAACAGATGGTCAAGCAAGTACT 120
QY 100 GGGAGGAGCGCCATCCTCTCTGTGGGCTACGGTTGCTACTGTGGCTGGGGGGCGGT 159
DB 121 GGGAAATGCCCATCTCTCTCTACTGGCCCTACGGCTGTCTACTGGGACTAGGTGGCAGA 180
QY 160 GGGCAACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
DB 181 GGGCAACCCCAAGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 240
QY 220 CTCCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAC 279
DB 241 CTGAGAGCCCGGGTGGCGAGCATCTACAAGGACTATTACAGATACAACTT-----TTCC 294

		Matches	202;	Conservative	0;	Mismatches	145;	Indels	6;	Gaps	1;
Qy	40	GTTCGTCCACAGCTCAGCGAGCTGCTCAACCTGAAGCCATGTGGAGCGCGTCA	99								
Db	57	GGTGTGATTCACATCCAGGGGGGATCTGAACTGACACAGATGGTCAAGCAAGT	116								
Qy	100	GGGAGGAGCGCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	159								
Db	117	GGGAAATGCCCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	176								
Qy	160	GGCCAGCCCAAGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	219								
Db	177	GGCCAAACCAAGATGAGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	236								
Qy	220	CTCTTTGACCAAGGTGTCACCCCTATGTGACCACTATGATACACCATCGAGA	279								
Db	237	CTGAAGACCCAGGTGGGTCATCTACAGGACTATTACAGATACAACTT-----	290								
Qy	280	ACTGAGATAGTTCGAGTGACCTCAACAGACAGAGTGTGACAGCAGACATG	339								
Db	291	CAGGGGAACATCCACTGCTCTGACAAAGGAGCTGGTGTGAGCAGCAGCTGT	350								
Qy	340	GACAAGACATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	392								
Db	351	GACAAGAGGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	403								
RESULT 8											
AAA77684											
ID AAA77684 standard; cDNA; 496 BP.											
AC AAA77684;											
XX 07-NOV-2000 (first entry)											
DE Human PRO1561 cDNA sequence SEQ ID NO:221.											
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;											
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;											
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;											
KW cytostatic; gene therapy; vaccine; ss.											
XX Homo sapiens.											
XX WO200032221-A2.											
XX 08-JUN-2000.											
XX 30-NOV-1999; 99WO-US28313.											
XX 01-DEC-1998; 98WO-US25108.											
XX 16-DEC-1998; 98US-0112850.											
XX 12-JAN-1999; 99US-0115554.											
XX 08-MAR-1999; 99WO-US05028.											
XX 12-MAR-1999; 99US-0123957.											
XX 28-APR-1999; 99US-0131445.											
XX 14-MAY-1999; 99US-0134287.											
XX 02-JUN-1999; 99WO-US12252.											
XX 23-JUN-1999; 99US-0141037.											
XX 26-JUL-1999; 99US-0144758.											
XX 01-SEP-1999; 99WO-US20111.											
XX 08-SEP-1999; 99WO-US20594.											
XX 13-SEP-1999; 99WO-US20944.											
XX 15-SEP-1999; 99WO-US21090.											
XX 05-OCT-1999; 99WO-US21547.											
XX 29-OCT-1999; 99WO-US23089.											
XX 99US-0162506.											
(GETH) GENENTECH INC.											
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;											
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;											

Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombolytic; antilipemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator; neuroprotectant; cerebroprotective; ds.

Homo sapiens.

Key Location/Qualifiers
CDS 18..455
/tag= a
/product= "Human CG95 (or C870) lipase protein"
FT sig_peptide 18..89
/tag= b
FT mat_peptide 90..452
/tag= c
/product= "Human mature CG95 (or C870) protein"

WO200179446-A2.

25-OCT-2001.

16-APR-2001; 2001WO-US12529.

14-APR-2000; 2000US-197137P.
20-JUN-2000; 2000US-0598042.
03-AUG-2000; 2000US-0631451.
22-SEP-2000; 2000US-0667298.
17-NOV-2000; 2000US-0714936.

(HYSE-) HYSEQ INC.

Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
Wang D;
WPT; 2001-611724/70.
P-PSDB; AAE11924.

Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein receptor polypeptides, useful for preventing diagnosing and treating lipid metabolism disorders, thrombosis and cardiovascular diseases -

Claim 1; Page 153-154; 266pp; English.

The invention relates to polynucleotides encoding proteins CG122, CG179, CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human apolipoproteins, lipases and lipoprotein receptor proteins. These DNA and protein sequences are useful for treating or preventing disorders associated with apolipoproteins, lipases and lipoprotein receptor (ALLr) expression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for determining the presence of or predisposition to a disease associated with altered levels of these sequences. ALLr polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALLr proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALLr proteins. The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular diseases, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, coronary artery thrombosis and cerebral artery thrombosis or intracardiac thrombosis and stroke. The nucleotides of the invention are used in gene therapy. The present sequence is human CG95 (or C870) lipase DNA.

Sequence 1931 BP; 417 A; 600 C; 479 G; 435 T; 0 other;

Query Match 19.5%; Score 99; DB 22; Length 1931;
Best Local Similarity 57.2%; Pred. No. 1.8e-15;


```

PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 22-SEP-1998; 98US-0101071.
PR 23-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103238.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 14-OCT-1998; 98US-0103711.
PR 20-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 21-OCT-1998; 98US-0105002.
PR 22-OCT-1998; 98US-0105169.
PR 26-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 28-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 29-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 30-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 10-NOV-1998; 98US-0106934.
PR 17-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.

PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX (GETH) GENENTECH INC.
XX PA
XX PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2000-237871/20.
DR P-PSDB; AAY99450.
XX DR
XX PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX PS Claim 2; Fig 22L; 773pp; English.
XX CC
XX CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX CC transmembrane and receptor PRO proteins can be used for screening of
XX CC potential peptide or small molecule inhibitors of the relevant
XX CC receptor/ligand interactions. The polypeptides and nucleotide sequences
XX CC encoding then have various industrial applications, including uses as
XX CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX CC PCR primers and hybridisation probes used in the isolation of the PRO
XX CC polypeptides from the present invention.
SQ Sequence 497 BP; 201 A; 95 C; 104 G; 95 T; 2 other;

Query Match 18.9%; Score 95.6; DB 21; Length 497;
Best Local Similarity 63.5%; Pred. No. 8.8e-15;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 40 GTTCTGTCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGCGGTCACA 99
Db 68 GGTGTGATTCCAATCCAGGGCGGATCCTCAACCTGAACAAGATGTCGAAGCAATGACT 127
Qy 100 GGGAGGAGCGCCATCCTCTCTTCTGGGGCTACGGTTGTCTACTGTGGTGGGGGGCGGT 159
Db 128 GGGAAATGGCCATCCCTCTCTACTGGCCCTACGGGTGCTCACTGCGGACTAGTGGCACA 187
Qy 160 GGCACGCCCAAGGATGAGGTGGACTGGTGTGCGCCAGCCCGCAGCTGCTGCTACCAAGNA 219
Db 188 GGCACACCCAAAGATGCCAGGACTGGTGTGCGCCAGCCCGCAGCTGCTGCTATGACCCAC 247
Qy 220 CTCTTTGACCAAGGTGTACCCCTATGTGGACCACTATGATCATCACACCAT 269
Db 248 CTGAAGACCCAGGGTGGCGCATCTACAAGGACAACAACAAAAGCAGCAT 297

RESULT 12
AAQ81136
ID AAQ81136 standard; cDNA; 4325 BP.
XX AC
XX AC AAQ81136;
XX DT
XX DT 15-AUG-1995 (first entry)
XX DE
XX DE RPLA2-8 gene.
XX XX

```

KW RPLA2-8; phospholipase A2; PLA2; Batten disease;
KW neuronal ceroid lipofuscinosis; gene therapy; ss.
XX
XX Rattus sp.

XX Key Location/Qualifiers
XX CDS 722..1198
XX /*tag= a

XX W09502328-A.

XX 26-JAN-1995.

XX 15-JUL-1994; 94WO-US07926.

XX 15-JUL-1993; 93US-0091941.

XX 26-JUL-1993; 93US-0097354.

XX (INCY-) INCYTE PHARM INC.

XX (INDV) UNIV INDIANA FOUND.

XX Seilhamer JJ, Tischfield JA;

XX WPI; 1995-067096/09.

XX P-PSDB; AAR63044.

XX Novel type III and IV low mol. wt. phospholipase A2 enzymes -
XX from humans and rats, also nucleic acid sequences useful, e.g.
XX PT for recombinant prodn. of enzymes, research into Batten's
XX PT disease, etc.

XX PS Disclosure; Page 57-60; 160pp; English.

XX A human PLA2-encoding cDNA (AAQ81137) expressing HPLA2-10, was
XX isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 cDNAs,
XX designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated
XX from rat brain and heart cDNA libraries, respectively. A partial human
XX genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained.
XX RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10
XX and HPLA2-10 as type IV.

XX Sequence 4325 BP; 1046 A; 1086 C; 1242 G; 951 T; 0 other;

Query Match 17.0%; Score 86.4; DB 16; Length 4325;
Best Local Similarity 60.0%; Pred. No. 3.6e-12;
Matches 144; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 47 CCACAGCTCAGCGAGCGCTGCTCAACCTGAGGCCATGGTGGAGCGGTCACAGGGAGGA 106
DB 792 COTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACACATCAGGGGGCGCA 851
QY 107 GGGCCATCTGTCCTGCTGGGCTACGCTTGTCTACTGTGGGCTGGGGCGCGTGGCCAGC 166
DB 852 GGGCCCTCTCTCCATTACGGATATGCTGCTACTGTGGGCTGGGGCGGAGGATCC 911
QY 167 CCAAGGATGAGTGGGACTGGTGTGCTGCCACGCCAGCAGTGTGCTACAGAACTCTTTG 226
DB 912 CTGTGGAGCCACAGACAGAGTGTCTGTGGGCTCATGATGTGTGTACCAAGCTTAAGG 971
QY 227 ACCAAGGTGTGTCACCCCTATGTGGACCACTATGATCACCACATCGAGAACACACTGAGA 286
DB 972 AATATGGCTGGCAGGCCCATCTTGAATGCTATCAGTTTGCAGTTGTCAACGGGACCGTGA 1031

RESULT 13
AAQ81137
ID AAQ81137 standard; cDNA; 1828 BP.

XX AAQ81137;
XX AC
XX DT 15-AUG-1995 (first entry)
XX XX
XX DE RPLA2-10 gene.

XX RPLA2-10; phospholipase A2; PLA2; Batten disease;
KW neuronal ceroid lipofuscinosis; gene therapy; ss.
XX
XX Rattus sp.

XX Key Location/Qualifiers
XX CDS 233..646
XX /*tag= a

XX W09502328-A.

XX 26-JAN-1995.

XX 15-JUL-1994; 94WO-US07926.

XX 15-JUL-1993; 93US-0091941.

XX 26-JUL-1993; 93US-0097354.

XX (INCY-) INCYTE PHARM INC.

XX (INDV) UNIV INDIANA FOUND.

XX Seilhamer JJ, Tischfield JA;

XX WPI; 1995-067096/09.

XX P-PSDB; AAR63045.

XX Novel type III and IV low mol. wt. phospholipase A2 enzymes -
XX from humans and rats, also nucleic acid sequences useful, e.g.
XX PT for recombinant prodn. of enzymes, research into Batten's
XX PT disease, etc.

XX PS Disclosure; Page 63-64; 160pp; English.

XX A human PLA2-encoding cDNA (AAQ81138) expressing HPLA2-10, was
XX isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 cDNAs,
XX designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated
XX from rat brain and heart cDNA libraries, respectively. A partial human
XX genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained.
XX RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10
XX and HPLA2-10 as type IV.

XX Sequence 1828 BP; 426 A; 485 C; 489 G; 428 T; 0 other;

Query Match 16.3%; Score 82.8; DB 16; Length 1828;
Best Local Similarity 56.7%; Pred. No. 2.3e-11;
Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1 ATCAAGAAGTTCTTCCCGTGGCCATCTTGTGTCGAGCGGTTTGTCTCCACAGCTCACGGC 60
DB 233 ATGAAGCGCTCTCTCAGCTGGCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
QY 61 AGCCTGCTCAACCTGAAGCCATGTGGAGCGGTACAGGGAGGAGCCCATCTCTGTC 120
DB 293 GGCTTGTCTAGAACTGAAGTCCATGATGAGAGGTGACTGGGGAAGTCCGCTTAAGAAC 352
QY 121 TTGCTGGGCTACGCTTGTCTACTGTGGGCGCGCTGGCCAGCCAGGATGAGGTG 180
DB 353 TATGGCTTCTACGGCTGCTACTGTGCTGGGCGGCCACGGGACCCCTTAAGGATGCACT 412
QY 181 GACTGTGTGCTGCCACGCCACGACTGCTGTCTACAGAACTCTTTGACCAAGGCTGTAC 240
DB 413 GATTGTGTGCTGCTGGATGTCAGACCGCTTGTATGGGCTACTGGAGGAGAAACACTGTGCC 472

QY 241 CCCTATGTGGACCACTATGATCATCACCATC 270
DB 473 ATCCGGACCCAGTCCCTATGACTACAGATTC 502

RESULT 14
AAQ72076
ID AAQ72076 standard; cDNA; 1233 BP.

XX

AC	AAAT72076;
XX	
DT	24-NOV-2000 (first entry)
XX	
DE	cDNA encoding mouse secreted phospholipase A2.
XX	
KW	Secreted phospholipase A2; PLA2; mouse; murine; recombinant production; antibody; diagnosis; expressed sequence tag; EST; drug screening; ss.
XX	
OS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	CDS 36..470
FT	/tag= a
FT	/product= "Mouse secreted phospholipase A2"
FT	36..92
FT	/tag= b
FT	mat_peptide 93..467
FT	/tag= c
FT	/product= "Mouse mature secreted phospholipase A2"
XX	
PN	JP2000166544-A.
XX	
PD	20-JUN-2000.
XX	
PF	09-DEC-1998; 98JP-0349602.
XX	
PR	09-DEC-1998; 98JP-0349602.
XX	
PA	(SHIO) SHIONOGI & CO LTD.
XX	
WP	WIPI; 2000-458171/40.
DR	P-PSDB; AAB11994.
XX	
PT	Mouse secretion type phospholipase A2 -
XX	
PS	Claim 5; Page 8-10; 12pp; Japanese.
XX	
CC	This sequence represents cDNA encoding a mouse secreted phospholipase A2 (secreted PLA2). This was initially identified in an EST (expressed sequence tag) database, and a fragment (AAAT72077) was isolated from cDNA derived from several mouse tissue types using primers AAAT72078-A72081. The full length cDNA was generated using PLA2, nucleic acids encoding it, and variants of the protein which retain phospholipase A2 activity. It also encompasses an expression vector and host cells comprising DNA encoding murine secreted PLA2, a method for the recombinant production of the protein, a method of screening potential inhibitors of the protein and the compounds thus identified, and an antibody specific for murine PLA2. The antibody can be used for the diagnosis of a variety of diseases.
SQ	Sequence 1233 BP; 279 A; 337 C; 307 G; 310 T; 0 other;
Query Match	16.3%; Score 82.4; DB 21; Length 1233;
Best Local Similarity	54.2%; Pred. No. 2 6e-11;
Matches 192; Conservative	0; Mismatches 156; Indels 6; Gaps 1;
QY	39 CGTCTGTGTCACAGCTCAGCGCACCTGCTCAACCTGAAGGCCATGGTGAGGCGGTCAAC 98
Ddb	71 CGGTATAACTGCACCCAGGGGGGCTCTGAACCTGAACAGATGGTCACACACATGAC 130
QY	99 AGGGAGGAGGCCCATCTCTGCTTCTGTGGGCTACGGTTGCTACTGTGGCTGGGGGGCG 158
Ddb	131 GGGGAAGAAGCCCTTCTTCAGCTACTGGCCCTACGGCTGTCACTGTGGACTTGGTGGCAA 190
QY	159 TGCGCAGCCCCAAGATGAGGTGAGTGTGTGCTGCCACGCCACGACTGCTGCTACCAGGA 218
Ddb	191 AGGGCAACCCAAAAGATGCCACAGACTGGTCTGTCAAGACGATGATTGTGCTATGCCCA 250
QY	219 ACTCTTTTGACCAAGGCTGTGCACCCCCTATGTGGACCACTATGATCACACATCGAGAACAA 278
Ddb	251 CCTGAAGATCGATGGATGCAAGACGCTGCACAGACTACAATAACAGCATCTCCACGG 310

us-09-975-456b-1.rng

Mon Feb 10 11:35:46 2003

```
QY 39 CGTTCTGTCCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCAC 98
Db 71 CGGTATAACTGCNAACCCAGGGAGGCTCCTGAACCTGAACAAAGATGGTCACACACATGAC 130
QY 99 AGGGAGAGCGGCCATCCTGTCCCTTGTGGCTACGGTTGCTACTGTGGGCTGGGGGCGG 158
Db 131 GGGGAAGAAAGCCTTCTCAGCTACTTGGCCCTACGGCTGTCTACTGTGGACTTGGTGGCAA 190
QY 159 TGGCCAGCCCAAGGATGAGGTGACTGTGTGCTGCCACGCCACGACTGCTGTACACAGGA 218
Db 191 AGGGCAACCCAAAGATGCCACAGACTGGTGTGCTCAGAAGCATGATTGTTGCTATGCCCA 250
QY 219 ACTCTTTTGACCAAGGCTGTCCACCCCTATGTGGACCCTATGATCACCACCATCGAACA 278
Db 251 CCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACACTACAATACAGCATCTCCAGGG 310
QY 279 CACTGAGATAGTCTGCAGTGACCTCAACAGACAGAGTGTGACAAGCAGACATGTCATGTG 338
Db 311 CACT-----ATCCAGTGTCTGACAAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTG 364
QY 339 TGACAAGAATGGTCTGTGCTGCTCATGAACACAGAGTACCGAGAGGAGTACCG 392
Db 365 TGACAAGGAGTGGCCTTGTGCTTGAAGCAAAACCTGGATAGCTACAATAAGCG 418
```

Search completed: February 8, 2003, 04:30:03
Job time : 232 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:30:09 ; Search time 47 Seconds
(without alignments)

Title: US-09-975-456B-1
Perfect score: 507
Sequence: 1 atgaagaagtcttcacgt.....cgcccccgccctccctag 507
3308.194 Million cell updates/sec

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	88	17.4	4325	2	US-08-888-497-21	Sequence 21, Appl
2	88	17.4	4325	4	US-09-362-230-21	Sequence 21, Appl
3	88	17.4	4325	5	PCT-US94-07926-21	Sequence 21, Appl
4	82.8	16.3	1828	2	US-08-888-497-29	Sequence 29, Appl
5	82.8	16.3	1828	4	US-09-362-230-29	Sequence 29, Appl
6	82.8	16.3	1828	5	PCT-US94-07926-29	Sequence 29, Appl
7	76.8	15.1	1014	2	US-08-888-497-31	Sequence 31, Appl
8	76.8	15.1	1014	4	US-09-362-230-31	Sequence 31, Appl
9	76.8	15.1	1014	5	PCT-US94-07926-31	Sequence 31, Appl
10	75.8	15.0	742	3	US-08-966-317-2	Sequence 2, Appl
11	75.8	15.0	742	4	US-09-489-770-2	Sequence 2, Appl
12	57.8	11.4	479	1	US-08-186-895-9	Sequence 2, Appl
13	54	10.7	151	2	US-08-888-497-26	Sequence 9, Appl
14	54	10.7	151	4	US-09-362-230-26	Sequence 26, Appl
15	54	10.7	151	5	PCT-US94-07926-26	Sequence 26, Appl
16	48.2	9.5	15328	2	US-08-888-497-33	Sequence 33, Appl
17	48.2	9.5	15328	4	US-09-362-230-33	Sequence 33, Appl
18	48.2	9.5	15328	5	PCT-US94-07926-33	Sequence 33, Appl
19	47.6	9.4	151	2	US-08-888-497-25	Sequence 25, Appl
20	47.6	9.4	151	4	US-09-362-230-25	Sequence 25, Appl
21	47.6	9.4	151	5	PCT-US94-07926-25	Sequence 25, Appl
22	40.8	8.0	5163	3	US-08-700-651-1	Sequence 1, Appl
23	40.8	8.0	5163	3	US-08-928-361B-4	Sequence 4, Appl
24	40.8	8.0	5318	3	US-08-700-651-2	Sequence 2, Appl
25	40.8	8.0	5318	3	US-08-928-361B-3	Sequence 3, Appl
26	36.8	7.3	536	4	US-09-465-558-33	Sequence 33, Appl
27	36.6	7.2	1288	1	US-08-440-856A-9	Sequence 9, Appl

28	36.6	7.2	5511	3	US-08-928-361B-2	Sequence 2, Appl
29	36.6	7.2	7334	3	US-08-928-361B-1	Sequence 1, Appl
30	36.2	7.1	1187	1	US-08-440-856A-2	Sequence 2, Appl
31	35.6	7.0	3468	1	US-07-951-715A-2	Sequence 2, Appl
32	35.6	7.0	3468	2	US-08-459-448A-2	Sequence 2, Appl
33	35.6	7.0	3468	3	US-08-459-595A-2	Sequence 2, Appl
34	35.6	7.0	3468	3	US-08-459-504B-2	Sequence 2, Appl
35	35.6	7.0	3468	3	US-08-459-444-2	Sequence 2, Appl
36	35.6	7.0	3468	3	US-09-053-549-3	Sequence 2, Appl
37	35.6	7.0	3468	4	US-09-547-422-2	Sequence 3, Appl
38	35.6	7.0	4523	4	US-09-473-716-1	Sequence 2, Appl
39	35.2	6.9	360	4	US-09-060-756-455	Sequence 455, App
40	35.2	6.9	1920	4	US-09-160-496-4	Sequence 4, Appl
41	35	6.9	1806	2	US-08-980-060-1	Sequence 1, Appl
42	35	6.9	1806	4	US-09-307-185-1	Sequence 1, Appl
43	35	6.9	3459	2	US-08-980-060-3	Sequence 3, Appl
44	35	6.9	3459	4	US-09-307-185-3	Sequence 3, Appl
45	34.4	6.8	13842	4	US-09-105-537-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-888-497-21
; Sequence 21, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: Mamalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSES: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS

US-09-362-230-21
LOCATION: 722..1195
NAME/KEY: CDS
LOCATION: 722..1195
US-09-362-230-21
Query Match 17.4%; Score 88; DB 4; Length 4325;
Best Local Similarity 60.4%; Pred. No. 2e-14;
Matches 145; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 47 CCACAGCTCAGCGCAGCTGCTCAACCTGAAGCCATGTTGGAGGCGCTCAAGGGAGGA 106
DB 792 CCTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACACATCACGGGGCGCA 851
QY 107 GCGCCATCTGCTCTGCTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGCGCCAGC 166
DB 852 GCGCTTCTTCTCTATTACGGATATGGCTGCTACTGTGGGCTTGGGGCGGAGGATCC 911
QY 167 CAAGGATGAGTGGAGTGTGCTGCCAGCCACGACTGCTGCTACCAAGAACTCTTTG 226
DB 912 CTGTGGAGCCACAGACAGTGTGCTGGGCTCATGACTGTTGCTACCAAGCTTAAGG 971
QY 227 ACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCACGAGACACACTGAGA 286
DB 972 AATATGCTGCCAGCCACTTCTGAATGCTATCATGTTGCCATTGTCAACGGGACCGTGA 1031
RESULT 3
PCT-US94-07926-21
Sequence 21, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 722..1195

US-08-888-497-21
LOCATION: 722..1195
NAME/KEY: CDS
LOCATION: 722..1195
US-08-888-497-21
Query Match 17.4%; Score 88; DB 2; Length 4325;
Best Local Similarity 60.4%; Pred. No. 2e-14;
Matches 145; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 47 CCACAGCTCAGCGCAGCTGCTCAACCTGAAGCCATGTTGGAGGCGCTCAAGGGAGGA 106
DB 792 CCTCCACCTCAGCAGCTTCTGGCAGTTCACAGAGGATGGTCAACACATCACGGGGCGCA 851
QY 107 GCGCCATCTGCTCTGCTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGCGCCAGC 166
DB 852 GCGCTTCTTCTCTATTACGGATATGGCTGCTACTGTGGGCTTGGGGCGGAGGATCC 911
QY 167 CAAGGATGAGTGGAGTGTGCTGCCAGCCACGACTGCTGCTACCAAGAACTCTTTG 226
DB 912 CTGTGGAGCCACAGACAGTGTGCTGGGCTCATGACTGTTGCTACCAAGCTTAAGG 971
QY 227 ACCAAGGCTGTACCCCTATGTGGACCACTATGATCACCACGAGACACACTGAGA 286
DB 972 AATATGCTGCCAGCCACTTCTGAATGCTATCATGTTGCCATTGTCAACGGGACCGTGA 1031
RESULT 2
US-09-362-230-21
Sequence 21, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 233..643
US-09-362-230-29

Query Match 16.3%; Score 82.8; DB 4; Length 1828;
Best Local Similarity 56.7%; Pred. No. 3.7e-13;
Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGCTGGCAGCGTCTTGTCCACAGCTCAGGC 60
DB 233 ATGAAGCGCTCTTACCGTGGCCATCCTTGTGCTGGCAGCGTCTTGTCCACAGCTCAGGC 292
QY 61 AGCCTGCTCAACCTGAAGCCATGTTGAGCGCTGCACAGGAGGAGCGCCATCCTGTCC 120
DB 293 GCGTTGCTAGAAGTGAAGTCCATGATTGAGAGTGACTGGGAAGATGCGGTAAGAAG 352
QY 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGCGGCGGCGGCGGCGGCGG 180
DB 353 TATGGCTTCTACGGCTGCTACTGTGGCTGGGGCGGCGGCGGCGGCGGCGGCGGCGG 412
QY 181 GACTGGTGTGCCAGCCAGCAGCTGCTGTACAGGAACTCTTTGACCAAGGCTGTCC 240
DB 413 GATTGGTGTGCTGCGATGCGACAGCGTGTGTTATGGGCTACTGGAGGAGAAACACTGTGCC 472
QY 241 CCCTATGTGGACCACTATGATCACACCATC 270
DB 473 ATCCGGACCCAGTCTTATGACTACAGATTC 502

RESULT 6

PCT-US94-07926-29
Sequence 29, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:

LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 233..643
PCT-US94-07926-29

Query Match 16.3%; Score 82.8; DB 5; Length 1828;
Best Local Similarity 56.7%; Pred. No. 3.7e-13;
Matches 153; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGCTGGCAGCGTCTTGTCCACAGCTCAGGC 60
DB 233 ATGAAGCGCTCTTACCGTGGCCATCCTTGTGCTGGCAGCGTCTTGTCCACAGCTCAGGC 292
QY 61 AGCCTGCTCAACCTGAAGCCATGTTGAGCGCTGCACAGGAGGAGCGCCATCCTGTCC 120
DB 293 GCGTTGCTAGAAGTGAAGTCCATGATTGAGAGTGACTGGGAAGATGCGGTAAGAAG 352
QY 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGGCGGCGGCGGCGGCGGCGG 180
DB 353 TATGGCTTCTACGGCTGCTACTGTGGCTGGGGCGGCGGCGGCGGCGGCGGCGGCGG 412
QY 181 GACTGGTGTGCCAGCCAGCAGCTGCTGTACAGGAACTCTTTGACCAAGGCTGTCC 240
DB 413 GATTGGTGTGCTGCGATGCGACAGCGTGTGTTATGGGCTACTGGAGGAGAAACACTGTGCC 472
QY 241 CCCTATGTGGACCACTATGATCACACCATC 270
DB 473 ATCCGGACCCAGTCTTATGACTACAGATTC 502

RESULT 7

US-08-888-497-31
Sequence 31, Application US/08888497
Patent No. 5972677
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5

TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 131..544
US-08-888-497-31

Query Match 15.1%; Score 76.8; DB 2; Length 1014;
Best Local Similarity 57.5%; Pred. No. 1.2e-11;
Matches 138; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
Qy 1 ATGAAGAAGTTCTTCACCGTGGCCATCTTGTGGCAGCGTTCCTGCTCCACAGCTCAGCGC 60
Db 131 ATGAAGGCGCTCTCCACCTGGCTTGGTTCTTGTAGTGTGCTGCTGTGCAAGGA 190
Qy 61 AGCTGCTCAACCTGAAGGCGTGGAGGCGGTGACAGGAGGAGGCCCATCTCTGTGCC 120
Db 191 GGCTTGTGGACCTTAAATCAATGATCGAGAGGTGACAGGAGGAGGCCCTGACAAAC 250
Qy 121 TTCTGGGCTACGTTGCTACTGTGGCTGGGGGCGGTGGCCAGGCGCCCAAGGATGAGGTG 180
Db 251 TACGGCTTCTACGGCTGTACTCGGCTGGGGGCGGTGGCCAGGAGGAGGCCCATCTCTGTGCC 310
Qy 181 GACTGTGCTGCCAGCGCCAGCACTGCTGTACAGGAACCTTTTGACCAAGGCTGTGCAC 240
Db 311 GATTGGTGTGTTGGCGCATGACCACTGCTATGGCGCGCTGGAGGAGGAGGCTGCAAC 370

RESULT 8
US-09-362-230-31
Sequence 31, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSER: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/362,230
APPLICATION NUMBER: US/09/362,230
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264

REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 131..544
US-09-362-230-31

Query Match 15.1%; Score 76.8; DB 4; Length 1014;
Best Local Similarity 57.5%; Pred. No. 1.2e-11;
Matches 138; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
Qy 1 ATGAAGAAGTTCTTCACCGTGGCCATCTTGTGGCAGCGTTCCTGCTCCACAGCTCAGCGC 60
Db 131 ATGAAGGCGCTCTCCACCTGGCTTGGTTCTTGTAGTGTGCTGCTGTGCAAGGA 190
Qy 61 AGCTGCTCAACCTGAAGGCGTGGAGGCGGTGACAGGAGGAGGCCCATCTCTGTGCC 120
Db 191 GGCTTGTGGACCTTAAATCAATGATCGAGAGGTGACAGGAGGAGGCCCTGACAAAC 250
Qy 121 TTCTGGGCTACGTTGCTACTGTGGCTGGGGGCGGTGGCCAGGCGCCCAAGGATGAGGTG 180
Db 251 TACGGCTTCTACGGCTGTACTCGGCTGGGGGCGGTGGCCAGGAGGAGGCCCATCTCTGTGCC 310
Qy 181 GACTGTGCTGCCAGCGCCAGCACTGCTGTACAGGAACCTTTTGACCAAGGCTGTGCAC 240
Db 311 GATTGGTGTGTTGGCGCATGACCACTGCTATGGCGCGCTGGAGGAGGAGGCTGCAAC 370

RESULT 9
PCT-US94-07926-31
Sequence 31, Application PC/TUS9407926
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSER: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 15-JUL-1994
APPLICATION NUMBER: PCT/US94/07926
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:

RESULT 11
 US-09-489-770-2
 ; Sequence 2, Application US/09489770
 ; Patent NO. 6399301
 ; GENERAL INFORMATION:
 ; APPLICANT: Hawkins, Phillip R.
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/489,770
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/966,317
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0403 US

```

, , TELECOMMUNICATION INFORMATION:
, , TELEPHONE: 650-855-0555
, , TELEFAX: 650-845-4166
, , INFORMATION FOR SEQ ID NO: 2:
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 742 base pairs
, , TYPE: nucleic acid
, , STRANDEDNESS: single
, , TOPOLOGY: linear
, , IMMEDIATE SOURCE:
, , LIBRARY: OVARFUT01
, , CLONE: 816403
US-09-489-770-2

```

[illegible]

```

RESULT 12
US-08-186-895-9
; Sequence 9, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Vers
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993

```

: APPLICATION NUMBER: US/07/810,414
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kokullis, Paul N.
 : REGISTRATION NUMBER: 16,773
 : REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-861-3000
 : TELEFAX: 202-822-0944
 : TELEX: 6714627 CUSH
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 479 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: CDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 24..455
 : US-08-186-895-9

Query Match	11.4%	Score	57.8	DB 1	Length	479	
Best Local Similarity	52.2%	pred. No.	1.2e-06				
Matches	128	Conservative	0	Mismatches	117	Indels	0
						Gaps	0
QY	1	ATGAAGAAGTCTTCTTACCGTGGCCATCCTTCTGTGGCAGCGTTCTGTCCACAGCTCACGGC	60				
DB	24	ATGAAGACCCCTCTACTGTTGGCAGTGATCAGATCTTTTGGCCTACTGTCAGGCCCATGGG	83				
QY	61	AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTACACAGGAGGAGCCGCATCTCTGTCC	120				
DB	84	AATTTGGTGAATTTCCACAGAATGATCAAGTTGACGACAGGAAAGGACCCCATCTAGT	143				
QY	121	TTTCGTGGGCTACGGTPTGCTACTGTGGCTGGGGCGGTGGCCAGCCCAAGATGAGGTG	180				
DB	144	TATGGCTTCTACGGCTGCCACTGTGGCGTGGGTGGCAGAGGATCCCCCAAGGATCAACG	203				
QY	181	GACTGGTGGTCCAGGCCAGCATGTGCTACCAAGAACTCTTTGACCAGGCTGTCAAC	240				
DB	204	GATCGCTGCTGTGTCATCATGACTGTTGCTACAAACGCTCTGGAGAAACGTTGGATGTGCC	263				
QY	241	CCCTA	245				
DB	264	ACCAA	268				

```

RESULT 13
US-08-888-497-26
; Sequence 26, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSER: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497

```

```

FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
JUS-09-362-230-26

Query Match      10.7%; Score 54; DB 4; Length 151;
Best Local Similarity 61.3%; Pred. No. 8.5e-06;
Matches 87; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY      47 CCACAGCTACGGCAGCGCTGCTCAACTGAAGGCCATGCTGGAGGCCGTCACAGGGAGGA 106
Ddb      10 COTCCACCCTCAGCAGCTTCTGGCAGTTCCAGAGGATGGTCAAAACACATACACGGGCGCA 69

QY      107 GCGCATCTCTCTCTCTGCTGGGCTACGTTGCTACTGTGGCTGGGGGCCGTGGCCAGC 166
Ddb      70 GCGCCTCTCTCTCTCTATACGATATGGCTGCTACTGTGGGCTTGGGGCCGAGGGATCC 129

QY      167 CCAAGGATCAGGTGGACTGGTG 188
Ddb      130 CTGTGGACCCACAGACAGGTG 151

RESULT 15
PCT-US94-07926-26
; Sequence 26, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilbamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 26:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
PCT-US94-07926-26

```

```

Query Match      10.7%   Score 54;   DB 5;   Length 151;
Best Local Similarity 61.3%;   Pred. No. 8.5e-06;
Matches 87;   Conservative 0;   Mismatches 55;   Indels 0;   Gaps 0;

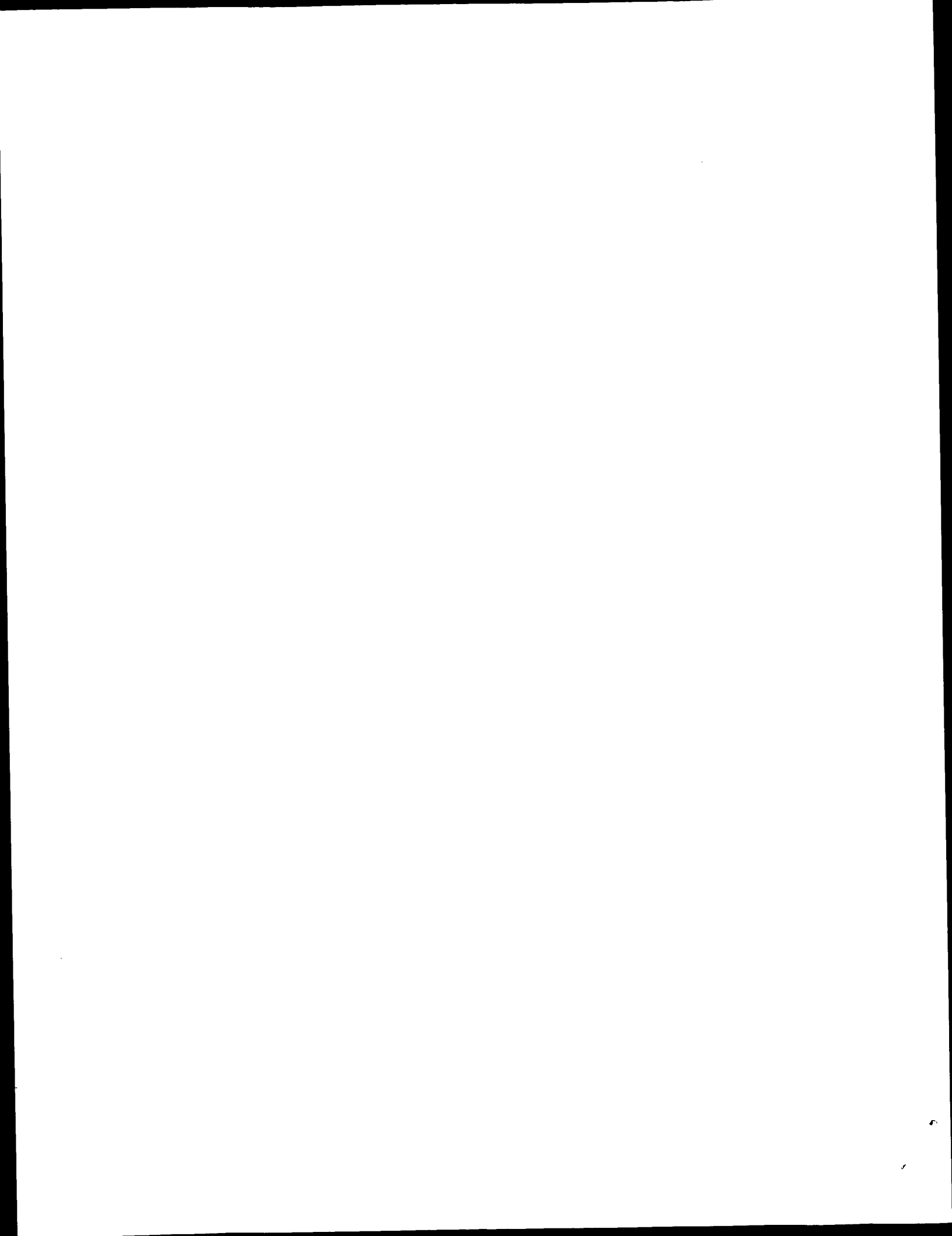
Qy  47 CCACAGCTCAGCGAGCGCTGCTCAACCTGAAGCCATGGTGGAGCGCTCACAGGGAGGA 106
Db  10 CCTCCACCTCAGCAGCTTCTGGCAGTTCCAGAGGATGGTCAACACATCACGGGGCGCA 69

Qy  107 GCGGCATCTCTCTTCGTTGGGCTACCGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGC 166
Db  70 GCGCCTTCTCTCTATACGGATATGGCTGCTACTGTGGCTTGGGGCCGAGGATCC 129

Qy  167 CCAAGGATGAGGTGGACTGGTG 188
Db  130 CTGTGGACGCCACACAGAGTG 151

```

Search completed: February 8, 2003, 06:39:31
Job time : 51 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 05:15:59 ; Search time 55 Seconds
(without alignments)
4369.446 Million cell updates/sec

Title: US-09-975-456B-1

Perfect score: 507

Sequence: 1 atgaagaagtcttcacgcg.....cgccccccgcccctccctag 507

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 - 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 - 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	19.5	854	9	US-09-969-384-6
2	99	19.5	1931	10	US-09-835-996A-5
3	95.6	18.9	496	9	US-10-028-072-533
4	95.6	18.9	496	9	US-10-121-049-533
5	95.6	18.9	496	9	US-10-123-904-533
6	95.6	18.9	496	9	US-10-140-470-533
7	75.8	15.0	742	9	US-10-124-591-2
8	65.8	13.0	445	10	US-09-962-832-63
9	57.8	11.4	854	10	US-09-969-708-597
10	57.8	11.4	1076	10	US-09-925-300-70
11	57.2	11.3	562	10	US-09-954-456-216
12	57.2	11.3	562	10	US-09-954-456-822
13	57.2	11.3	562	10	US-09-954-456-1225
14	57.2	11.3	630	10	US-09-925-297-52
15	55	10.8	854	10	US-09-765-231A-42
16	54	10.7	445	10	US-09-925-297-414
17	47.2	9.3	2310	10	US-09-476-242-3
18	44.8	8.8	3330	10	US-09-917-800A-1495
19	42	8.3	2310	10	US-09-476-242-21

20	42	8.3	2328	10	US-09-476-242-6	Sequence 6, Appl1
21	39.8	7.9	1790	9	US-09-905-370-2	Sequence 2, Appl1
22	39	7.7	2505	9	US-09-989-920-66	Sequence 66, Appl1
23	36.4	7.2	867	10	US-09-216-393-340	Sequence 340, App
24	36.4	7.2	867	10	US-09-216-393-342	Sequence 342, App
25	36.4	7.2	1397	10	US-09-216-393-343	Sequence 343, App
26	36.4	7.2	1397	10	US-09-216-393-345	Sequence 345, App
27	36.2	7.1	2322	10	US-09-476-242-18	Sequence 18, Appl
28	36.2	7.1	2322	10	US-09-476-242-19	Sequence 19, Appl
29	36.2	7.1	2322	10	US-09-476-242-20	Sequence 20, Appl
30	36.2	7.1	2334	10	US-09-476-242-7	Sequence 7, Appl1
31	36.2	7.1	2352	10	US-09-476-242-26	Sequence 26, Appl
32	36.2	7.1	2358	10	US-09-476-242-25	Sequence 25, Appl
33	36.2	7.1	2517	10	US-09-476-242-16	Sequence 16, Appl
34	36.2	7.1	2517	10	US-09-476-242-17	Sequence 17, Appl
35	36.2	7.1	2523	10	US-09-476-242-15	Sequence 15, Appl
36	36.2	7.1	2529	10	US-09-476-242-14	Sequence 14, Appl
37	36.2	7.1	2535	10	US-09-476-242-13	Sequence 13, Appl
38	36.2	7.1	2541	10	US-09-476-242-9	Sequence 9, Appl1
39	36.2	7.1	2541	10	US-09-476-242-10	Sequence 10, Appl
40	36.2	7.1	2541	10	US-09-476-242-11	Sequence 11, Appl
41	36.2	7.1	2541	10	US-09-476-242-12	Sequence 12, Appl
42	35.8	7.1	2298	10	US-09-476-242-22	Sequence 22, Appl
43	35.8	7.1	2298	10	US-09-476-242-24	Sequence 24, Appl
44	35.8	7.1	2316	10	US-09-476-242-4	Sequence 4, Appl1
45	35.8	7.1	2316	10	US-09-476-242-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1

US-09-969-384-6
; Sequence 6, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-384-6

Query Match 19.5%; Score 99; DB 9; Length 854;
Best Local Similarity 57.2%; Pred. No. 4.3e-18;
Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;
QY 40 GTTCTGTCACAGCTCAGCGGAGCTGCTCAACCTGGAAGGCGGCTGCTCAACAGTACT 99
DB 61 GGTGTGATTCCCAATCCAGGCGGGATCCTGAACCTGACAAAGTGGTCAACAGTACT 120
QY 100 GGGAGGAGCGCCATCCTGCTTCTGCTGGCTACGGTTCCTACTGTGGGCTGGGGGCGGT 159
DB 121 GGGAAAATGCCCATCCTCTCTACTGCGCCCTACGGCTGCTCACTCGGAGTGGGCGAGA 180
QY 160 GCCCAGCCCAAGGATGAGTGGGACTGGTGGCTGCCAGCCGACGACTGCTGCTACCGAGAA 219
DB 181 GCCCAACCCAAAGATGCCACGAGCTGGTGGCTGCCAGACCCATGACTGCTGCTATGACCAC 240
QY 220 CTCCTTGACCAAGGCTGTCCACCCCTATGTGGACCACTATGATACACCATCGAGCAAC 279

us-09-975-456b-1.l.rnpb

Mon Feb 10 11:35:47 2003

Db 237 CTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT-----TTCC 290
 QY 280 ACTGAGATAGTCTGACGTGACCTCAACAGACAGAGTGTGACAGCAGACATGATGTGT 339
 Db 291 CAGGGGAACATCCACTGCTGTGACAGAGGGAAGCTGTGTGACGACGACCTGTGTGCTGT 350
 QY 340 GACAAGAACATGTTCTGTGCTCATGAACACAGACGTAACCGAGAGGAGTACCG 392
 Db 351 GACAAGGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCAGAAGCG 403

RESULT 3

US-10-028-072-533
 ; Sequence 533, Application US/10028072
 ; Publication No. US20030004311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang
 ; TITLE OF INVENTION:
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/028,072
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059836
 ; PRIOR FILING DATE: 1997-09-24
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062285
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062814
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/062816
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063045
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063082
 ; PRIOR FILING DATE: 1997-10-31

Db 241 CTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT-----TTCC 294
 QY 280 ACTGAGATAGTCTGACGTGACCTCAACAGACAGAGTGTGACAGCAGACATGATGTGT 339
 Db 295 CAGGGGAACATCCACTGCTGTGACAGAGGGAAGCTGTGTGACGACGACCTGTGTGCTGT 354
 QY 340 GACAAGAACATGTTCTGTGCTCATGAACACAGACGTAACCGAGAGGAGTACCG 392
 Db 355 GACAAGGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCAGAAGCG 407

RESULT 2

US-09-835-996A-5
 ; Sequence 5, Application US/09835996A
 ; Patent No. US20020142953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ballinger, Dennis
 ; APPLICANT: Loeb, Debra
 ; APPLICANT: Montgomery, Julie
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhao, Qing
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Drmanac, Radoje
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Qian, Xiaohong
 ; APPLICANT: Wang, Durrui
 ; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
 ; FILE REFERENCE: 28110/35915A
 ; CURRENT APPLICATION NUMBER: US/09/835,996A
 ; CURRENT FILING DATE: 2001-04-16
 ; PRIOR APPLICATION NUMBER: US 60/197,137
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: US 09/714,936
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: US 09/667,298
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: US 09/631,451
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US 09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (18)..(452)
 ; US-09-835-996A-5

Query Match 19.5%; Score 99; DB 10; Length 1931;
 Best Local Similarity 57.2%; Pred. No. 5.8e-18;
 Matches 202; Conservative 0; Mismatches 145; Indels 6; Gaps 1;
 QY 40 GTTCTGTCACAGCTCACGGGAGCTGCTCAACCTGAAGGCCATGTTGGAGGCGCTCACA 99
 Db 57 GGTGTGATTCATCAATCAGGGCGGATCCTGAACCTGAACAGATGTTCAAGCAAGTGACT 116
 QY 100 GGAAGAGCGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 159
 Db 117 GGGAAATGCCATCTCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 176
 QY 160 GGCAGCGCCAAAGATGAGTGGAGTGGTGTGCTGCCAGCCAGCAGTGTGCTACCAAGGA 219
 Db 177 GGCACCCCAAGATGAGTGGAGTGGTGTGCTGCCAGCCAGCAGTGTGCTGCTATGACCA 236
 QY 220 CTCTTTGACCAAGGCTGTACCCCTATGTTGGACCACTATGATCACACCATCGAGAACAAC 279

; PRIOR APPLICATION NUMBER: 60/063127
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063327
 ; PRIOR FILING DATE: 1997-10-27
 ; PRIOR APPLICATION NUMBER: 60/063329
 ; PRIOR FILING DATE: 1997-10-27
 ; PRIOR APPLICATION NUMBER: 60/063550
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063561
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063704
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063733
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063735
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063738
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063755
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064248
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/064809
 ; PRIOR FILING DATE: 1997-11-07
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065846
 ; PRIOR FILING DATE: 1997-11-17
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/066453
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066511
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/069212
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069278
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069334
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069694
 ; PRIOR FILING DATE: 1997-12-16
 ; PRIOR APPLICATION NUMBER: 60/072320
 ; PRIOR FILING DATE: 1998-01-23
 ; PRIOR APPLICATION NUMBER: 60/073612
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: 60/074086
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074092
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/077791
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079663
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/080165
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081695
 ; PRIOR FILING DATE: 1998-04-14
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081818

; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082999
 ; PRIOR FILING DATE: 1998-04-24
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085149
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/086414
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/086430
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/088026
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088730
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088741
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088810
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088858
 ; PRIOR FILING DATE: 1998-06-11
 ; PRIOR APPLICATION NUMBER: 60/089532
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089599
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090429
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090445
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090538
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07

Query Match 18.9%; Score 95.6; DB 9; Length 496;
 Best Local Similarity 63.5%; Pred. No. 3e-17;
 Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Db	68	GGTGTGATTCCAAATCCAGGGGGGGATCTCGAACTGAAACAAGATGGTCAAGCAAGTGACT	127
QY	100	GGGAGGAGCGCCATCCTGTCTTCGTGGGCTACGGTTGTCTACTGTGGGCTGGGGGGCCGT	159
Db	128	GGGAAATGCCCATCCTCTCTACTACGGCTTACGGCTGTCACTCGGACTAGGTGGCAGA	187
QY	160	GGCCAGCCCAAGATGAGTGGAGCTGGTGTGCCACGCCACGACTGCTGCTACCCAGAA	219
Db	188	GGCCAAACCCAAAGATGCCAGGACTGGTGTGCCAGACCCCATGACTGCTGTATGACCAC	247
QY	220	CTCTTTGGCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCAT	269
Db	248	CTGAAGACCCAGGGTGGCGCATCTACAAGGACAAACAACAAAGCAGCAT	297
RESULT 4			
US-10-121-049-533			
; Sequence 533, Application US/10121049			
; Publication No. US2003002239A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: F3330R1C17			
; CURRENT APPLICATION NUMBER: US/10/121,049			
; CURRENT FILING DATE: 2002-04-12			
; Prior Application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 550			
; SEQ ID NO 533			
; LENGTH: 496			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: 396			
; OTHER INFORMATION: unknown base			
US-10-121-049-533			
Query Match 18.9%; Score 95.6; DB 9; Length 496;			
Best Local Similarity 63.5%; Pred. No. 3e-17;			
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps			
QY	40	GTTCTGTCCAGCTCAGGCGAGCCTCTCAACTGAAGCCCATGTGTGGAGCGCCGTTCACA	99
Db	68	GGTGTGATTCCAAATCCAGGGGGGGATCTGAACTGAAACAAGATGGTCAAGCAAGTGACT	127
QY	100	GGGAGGAGCGCCATCCTGTCTTCGTGGGCTACGGTTGTCTACTGTGGGCTGGGGGGCCGT	159
Db	128	GGGAAATGCCCATCCTCTCTACTACGGCTTACGGCTGTCACTCGGACTAGGTGGCAGA	187
QY	160	GGCAGGCCCAAGATGAGTGGAGCTGGTGTGCCACGCCACGACTGCTGCTACCCAGAA	219
Db	188	GGCCAAACCCAAAGATGCCAGGACTGGTGTGCCAGACCCCATGACTGCTGTATGACCAC	247
QY	220	CTCTTTGACCAAGGCTGTCAACCCCTATGTGGACCACTATGATCACACCAT	269

OPERATING SYSTEM: DOS

OPERATING SYSTEM: DOS

```

RESULT 8
US-09-962-832-63/c
: Sequence 63 Application US/09962832
: Patent No. US20020110821A1
: GENERAL INFORMATION:
: APPLICANT: Ebner, Reinhard
: TITLE OF INVENTION: Cancer Gene Determina
: FILE REFERENCE: 689290-74
: CURRENT APPLICATION NUMBER: US/09/962,832
: CURRENT FILING DATE: 2001-09-25
: PRIORITY APPLICATION NUMBER: US/60/235,077
: PRIORITY FILING DATE: 2000-09-25
: PRIORITY APPLICATION NUMBER: US/60/235,280
: PRIORITY FILING DATE: 2000-09-25
: NUMBER OF SEQ IDS: 259

```

```

RESULT 8
US-09-962-832-63/c
: Sequence 63 Application US/09962832
: Patent No. US20020110821A1
: GENERAL INFORMATION:
: APPLICANT: Ebner, Reinhard
: TITLE OF INVENTION: Cancer Gene Determina
: FILE REFERENCE: 689290-74
: CURRENT APPLICATION NUMBER: US/09/962,832
: CURRENT FILING DATE: 2001-09-25
: PRIORITY APPLICATION NUMBER: US/60/235,077
: PRIORITY FILING DATE: 2000-09-25
: PRIORITY APPLICATION NUMBER: US/60/235,280
: PRIORITY FILING DATE: 2000-09-25
: NUMBER OF SEQ IDS: 259

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or
US-09-962-832-63

```

Query Match

Query Match 13.0%; Score 65.8; DB 10; Length 445;
Best Local Similarity 52.6%;
Matches 171; Conservative 0; Mismatches 147; Indels 7; Gaps 1;

[illegible]

RESULT 9

US-09-969-708-597
; Sequence 597, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:

APPLICANT: Augustus

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-70

CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 560

0528 ID NO 391
LENGTH: 854

TYPE: DNA

ORGANISM: *Homosapiens*

5-09-969-708-597

```

Query Match          11.4%; Score 57.8; DB 10; Length 854;
Best Local Similarity 52.2%;
Matches 128; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

```

	Indels	Gaps	0;	0;
1 ATGACACACACCTTCCATC	II/;	0;	Gaps	0;

136 ATGAAGACCCCTCTACTCTTGGCAGTATCATCTTTGGCCTACTGCAGGCCCATGGG 195

61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTACAGGGAGGAGCGCCATCCTGTCC 120

100

١٠٠



1

Db	196	AATTTGGTGAATTTCCACAGAATGATCAAGTTGACGACAGGAAGAACGCCACTCAGT	255
Qy	121	TTGCTGGGCTACGGTTCTGCTACTGTGGCTGGGGGGCGGTGGCCAGCCCAAGGATGAGGTG	180
Db	256	TATGGCTTCTACGCGTGCCTGCTGTGGGTGGGTGGCAGAGGATCCCCAAGATGCAACG	315
Qy	181	GACTGTGTGTGCCACGCCACGACTGCTGTACCAAGAACTCTTTCACCAAGGCTGTGCAC	240
Db	316	GATCGCTGTGTGTCATCTGCTCATGACTGTTCTCTACAAACGCTCGGAGAAACGGTGTGGC	375
Qy	241	CCCTA	245
Db	376	ACCAA	380

RESULT 10

```

US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Protei
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

```

Query Match

Seq. ID	Seq. Type	Best Local Similarity	Score	DB 10	Length	1076;			
Matches	128;	Conservative	0;	Mismatches	117;	Indels	0;	Gaps	0;
1	ATGAAGAAGTTCTTCACCGTGGCCATCCTTGCTGGCAGCGTTCTGTGCACACGCTCACGGC	60	11.4%;	52.2%;	Pred. No. 1.1e-06;				
196	ATGAAGACCCCTCTACTGTGTGGAGTGATCATGATCTTTGGCCCTACTCGAGGCCCATGGG	255							
61	AGCCTGCTCAACCTGAAGGCATGTTGGAGGCCGCTCACAGGAGGAGCGCCATCCTGTGCC	120							
256	AATTTGTTGAATTTCCACAGATGATCAAGTTTGACGACAGGAAAGGACCGCACTCAGT	315							
121	TTCCGTGGGCTACGGTTGCTTACTGTGGGCTGGGGGCCGTGGCCACGCCAAGATGAGGTG	180							
316	TATGGCTTCTACGGCTGGCCACTGTGSCCTGGTGGCAGAGGATCCCCCAAGGATGCAACG	375							
181	GACTGTGTGCTGCCACGCCCACTGCTGCTTACAGGAACTTTTGTACCAAGCGCTGTAC	240							
376	GATCGCTGCTGTGTCACCTCATGACTGTGTGTGTACAAACGCTCTGGAGAAACGTGGATGTGGC	435							
241	CCCTA	245							
436	ACCA	440							

RESULT 11

US-09-954-456-216 ; Sequence 216, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:

QY 155 GCCGTGGCCAGCCAGGATGAGGTGGACTGGCTGCTGCCACGCCACGACTGCTGCTA 212
Db 201 GCTCAGGACCCCGCTGGATGAAGTGGACAGTGTGCCAGACATGACAACCTGCTA 258

RESULT 14

US-09-925-297-52
; Sequence 52, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL05
; CURRENT APPLICATION NUMBER: US/09/925,297
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (628)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-52

Query Match
Best Local Similarity 11.3%; Score 57.2; DB 10; Length 630;
Matches 80; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 95 TCACAGGAGGAGCGCCATCTGCTTCGTGGGTACGGTGTGCTACTGGGGTGGGG 154
Db 130 TCCCGGGAGTGACCCCTTCTTGAATACACAACTACGGCTGCTACTGGCTGGGG 189
QY 155 GCCGTGGCCAGCCAGGATGAGGTGGACTGGCTGCTGCCACGCCACGACTGCTGCTA 212
Db 190 GCTCAGGACCCCGCTGGATGAAGTGGACAGTGTGCCAGACATGACAACCTGCTA 247

RESULT 15

US-09-765-231A-42
; Sequence 42, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Phippard, Deborah
; APPLICANT: Vasanthakumur, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 42
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 1-854
; LOCATION: unknown
; OTHER INFORMATION: unsure at all n locations
US-09-765-231A-42

Query Match
Best Local Similarity 10.8%; Score 55; DB 10; Length 854;
Matches 115; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 1 ATGAAGAAGTTCTTCCACCGTGGCCATCCTTGTGGCAGCGTTCTGTCCACAGCTCAGGC 60
Db 149 ATGAAGACCCCTCCTACTGTGGCAGTGATCATGATCTTTGGCCTACTGCAGGCCCATGG 208
QY 61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTACACAGGAGGAGCGCCATCTGTGCC 120
Db 209 AATTTGGTGAATTTCCACAGAAATGATCAAGTTGACGACAGGAAAGGAGCGCCACTCAST 268
QY 121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGCCCTGGCCAGCCCCAAGGATGAGGTG 180
Db 269 TATGCTTCTACGGCTGCCACTGTGGCGTGGTGGCAGAGGATCCCCCAAGGATGCAACG 328
QY 181 GACTGGTGTGCCACGCCACGACTGCTGTACCA 215
Db 329 GATCGCTGCTGTGCTACTCATGACTGTTGTCTACAA 363

Search completed: February 8, 2003, 06:43:54
Job time : 58 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 02:43:59 ; Search time 1939 Seconds
(without alignments)
4234.715 Million cell updates/sec

Title: US-09-975-456b-1
Perfect score: 507
Sequence: 1 atgaagaagttcttcacgct.....cgccccccgcctccctccctag 507

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba:**
- 2: em_esthm:**
- 3: em_estin:**
- 4: em_estmu:**
- 5: em_estov:**
- 6: em_estpl:**
- 7: em_estro:**
- 8: em_estc:**
- 9: gb_estli:**
- 10: gb_est2:**
- 11: gb_htc:**
- 12: gb_est3:**
- 13: gb_est4:**
- 14: gb_est5:**
- 15: em_estfun:**
- 16: em_estom:**
- 17: gb_gss:**
- 18: em_gss_hum:**
- 19: em_gss_inv:**
- 20: em_gss_pln:**
- 21: em_gss_vrt:**
- 22: em_gss_fun:**
- 23: em_gss_mam:**
- 24: em_gss_mus:**
- 25: em_gss_other:**
- 26: em_gss_pro:**
- 27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255.4	50.4	657	10	BB613865
2	186.4	36.8	511	9	BB613865
3	167.8	33.1	486	9	AI173803
4	165.2	32.6	484	9	AI931322
5	146	28.8	452	9	AI574411
6	138	27.2	455	10	AI173890
					AW106043
					um22d03.y

7	99.6	19.6	463	13	BM153087
8	99.2	19.6	533	10	AW213414
9	94.6	18.7	484	13	BM106914
10	91.2	18.3	950	12	BF781906
11	91.2	18.0	680	13	BI836812
12	89.2	17.6	392	10	AW659630
13	89.2	17.6	558	13	BM363855
14	88.4	17.4	495	12	BF077514
15	83	16.4	460	9	AI430241
16	82.4	16.3	367	10	BB69347
17	82.4	16.3	472	10	BE138146
18	82.4	16.3	1582	11	AK018005
19	82	16.2	501	9	AA762051
20	81.8	16.1	446	14	BQ570398
21	81	16.0	1206	11	AK004232
22	79.6	15.7	620	9	AL660516
23	79.4	15.7	601	14	BQ418599
24	77.6	15.3	544	10	BE015249
25	75.8	15.0	543	10	AW292929
26	75.8	15.0	558	13	BM087924
27	75.4	14.9	909	12	BG293389
28	73.8	14.6	432	10	BB850720
29	73.6	14.5	442	9	AI769633
30	73.4	14.5	235	10	BE477104
31	71.8	14.2	666	10	AW918786
32	70.2	13.8	323	14	BM688463
33	70.2	13.8	447	14	BM688506
34	70	13.8	233	10	AW418175
35	68.2	13.5	388	12	BF150826
36	68	13.4	428	10	BB849474
37	66.6	13.1	356	10	BB868695
38	65.8	13.0	445	14	N93958
39	65.4	12.9	587	10	BB615766
40	65.4	12.9	834	13	BG964576
41	64.8	12.8	1590	14	BM926265
42	64.4	12.7	381	10	BE128774
43	64.2	12.7	396	10	AV691515
44	64.2	12.7	398	10	AV695929
45	64.2	12.7	410	10	AV698272

ALIGNMENTS

RESULT 1
BB613865
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BB613865
musculus
BB613865
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 657)

BB613865.1 GI:153955682

657 bp mRNA linear EST 31-AUG-2001
RIKEN full-length enriched, 0 day neonate head Mus
CDNA clone 4831444E21 5', mRNA sequence.
RIKEN
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

TITLE
JOURNAL
COMMENT

BB613865
musculus
BB613865
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 657)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,T., Toyama,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

BM153087 TCBAPIQ13
AW213414 um55d06.y
BM106914 510989.MA
BF781906 602105856
BI836812 603084703
AW659630 97101.MAR
BM363855 BS3200330
BF077514 227437.MA
AI430241 vv49h02.y
BB869347 BB869347
BE138146 ug49a11.y
AK018005 Mus muscu
AA762051 vv49h02.f
BQ570398 g1149c02.
AK004232 Mus muscu
AL660516 AL660516
BQ418599 lk55a07.y
BE015249 127486.MA
AW292929 UT-H-BW0-
BM087924 S01240.MA
BG293389 602390789
BB850720 BB850720
AI769633 wj25a06.x
BE477104 160561.BA
AW918786 EST350090
BM688463 UT-E-CRO-
BM688506 UT-E-CRO-
AW18175 55737.MAR
BF150826 uy86e10.y
BB849474 BB849474
BB868695 BB868695
N93958 zb74f04.s1
BB615766 BB615766
BG964576 602832255
BM926265 AGENCOURT
BE128774 DEPA2524
AV691515 AV691515
AV695929 AV695929
AV698272 AV698272

IMAGE Consortium (info@image.llnl.gov) for further information.
 MG1:1005481

Seq primer: custom primer used
 High quality sequence stop: 440.

FEATURES

Location/Qualifiers
 1. .455
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2225285"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTTAAAGTCGCG and 3' end primer CGACCTGCAGCTCGAGCACA." 91 t

BASE COUNT 97 a 137 c 130 g 91 t

Query Match 27.2%; Score 138; DB 10; Length 455;
 Best Local Similarity 82.5%; Pred. No. 3.7e-24;
 Matches 170; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 1 ATGAAGAAGTTCTTACCGTGGCCATCCTTGTGGCAGCGTCTGTCCACAGCTCAGCGC 60
 Db 251 ATGAAGAAGTTCTTGTGGCAGCGTCTGTCCACAGCTCAGCGC 60
 QY 61 AGCTGTCTCAACCTGAGGCCATGGTGGAGCGGTCTACAGGGAGGAGCGCCATCCTGTGC 120
 Db 311 AGCTGTCTCAACCTGAGGCCATGGTGGAGCGGTCTACAGGGAGGAGCGCCATCCTGTGC 120
 QY 121 TCTGTGGCTACGGTGTCTACTGTGGGCGGTGGCGGCGGTCTACAGGGAGGAGCGCGCCATCCTGTGC 180
 Db 371 TTTGTGGCTACGGTGTCTACTGTGGGCGGTGGCGGCGGTCTACAGGGAGGAGCGCGCCATCCTGTGC 180
 QY 181 GACTGTGTCTGCGCCAGCCCGCAGACTG 206
 Db 430 GACTGTGTCTGCGCCAGCCCGCAGACTG 455

RESULT 7

BM153087

LOCUS

DEFINITION

TCBAP1Q13560 Pediatric pre-B cell acute lymphoblastic leukemia

sequence.

BM153087

BM153087.1 GI:17177919

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 463)

Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R., Jr.,

Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.

Pediatric Leukemia cDNA Sequencing Project (2001)

Unpublished (2001)

Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center

at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

FEATURES

Location/Qualifiers
 1. .463
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TCBAP1356"
 /clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"
 /sex="male"
 /tissue_type="leukopheresis"
 /dev_stage="pre-B cell"
 /lab_host="DH10B"
 /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCCGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dc primer [5'AGAGCTCGATCGCGCGGCATTAATAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, high efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

BASE COUNT 104 a 125 c 137 g 97 t

Query Match 19.6%; Score 99.6; DB 13; Length 463;
 Best Local Similarity 57.4%; Pred. No. 1.4e-14;
 Matches 202; Conservative 0; Mismatches 144; Indels 6; Gaps 1;

QY 41 TTCTGTCCACAGCTCAGCGGAGCGTGTCAACCTGAAGGCCATGGTGGAGCGGTGCACAG 100
 Db 100 TTGTGATTTCAATCAGGGGGGATCCTGAACCTGAACAGAGTGTCAAGCAAGTGTACTG 159
 QY 101 GGAGGAGCGCATCTCTCTGTGGGTACGGTGTCTACTGTGGCTGGGGGGCGGTG 160
 Db 160 GGAAATGCCCCCTCTCTCTGTGGGTACGGGTGTCACTGCGGACTAGGTGGCAGAG 219
 QY 161 GCCAGCCAAAGATGCGCAGCGACTGGTGTGTGTCACCGCCCGCAGCTGCTCTACCGAGAAC 220
 Db 220 GCCAACCCAAAGATGCGCAGCGACTGGTGTGTGTCACCGCCCGCAGCTGCTCTATGACCACC 279
 QY 221 TCITTTGACCAAGCTGTACCCCTATGTGGACCATATGATCACCACATCGAGAACAAACA 280
 Db 280 TGAAGACCCAGGGGTGGCGGACTTACAAAGGACTATTACAGATACAACTT-----TTCCC 333
 QY 281 CTGAGATAGTCTGCAGTGTACCTCAACAAGAGAGTGTGACAGAGAGATCATGTGTG 340
 Db 334 AGGGAAATCCTCACTGCTGACAGGGAAGTGTGTGAGCAGGAGTGTGTGCTGTG 393
 QY 341 ACAAGAACATGTTCTGTGCTCATGAACACGACGTACCGAGGAGGTACCG 392
 Db 394 ACAAGAGGTGGCTTCTTCTGCTGAAGCGCAACCTTGACACCTTACCAGAGCG 445

RESULT 8

AW213414

LOCUS

DEFINITION

um53d06.y1 Sugano mouse embryo mewa Mus musculus cDNA clone

IMAGE:2259179 5', mRNA sequence.

AW213414

AW213414.1 GI:6519614

EST.

SOURCE

house mouse.

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AW213414 533 bp mRNA linear EST 15-MAR-2000
 um53d06.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:2259179 5', mRNA sequence.

AW213414
 AW213414.1 GI:6519614

EST.
 house mouse.

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mon Feb 10 11:35:50 2003

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 533)
 REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, K., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 TITLE
 JOURNAL
 COMMENT
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1007887
 Seq primer: custom primer used
 High quality sequence stop: 465.
 Location/Qualifiers
 FEATURES
 source
 1..533
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2259179"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CCCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end primer CGACTCGAGCTCGAGCACA."
 BASE COUNT 120 a 155 c 146 g 109 t 3 others
 ORIGIN
 Query Match 19.6%; Score 99.2; DB 10; Length 533;
 Best Local Similarity 80.1%; Pred. No. 1.9e-14;
 Matches 141; Conservative 0; Mismatches 33; Indels 2; Gaps 2;
 QY 1 ATCAAGAGTCTTCACCGTGGCCATCTTGTCTGGCAGCGTCTGTCCACAGCTCACGGC 60
 Db 246 ATGAAGAAATTTCTTGCATTCGAGTCTCTGGCGGAGTGTGTTACACACGCGCCACAGC 305
 QY 61 AGCCTGCTCAACCTGAAGGCGCATGGTGGAGGCGGTCTCACAGGAGGAGGCGCCA-TCTGTGTC 119
 Db 306 AGCCTGCTGAACCTGAAGTCCATGGTGGAGGCGCATCACACAGAACTCCATTCCTGTC 365
 QY 120 CTTGCTGGGCTAGGTTGCTTACTGTGGGCTGGG-GGGCGTGGCCAGCCCAAGGAT 174
 Db 366 CTTTGTGGGCTACGGTGTCTACTGTGGGCTGGGNGGAGCCGCGCATCCCATGGAT 421
 RESULT 9
 BM106914 484 bp mRNA linear EST 21-NOV-2001
 LOCUS
 DEFINITION 510989 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION
 VERSION BM106914.1 G1:17037984
 KEYWORDS
 EST.
 SOURCE
 Bos taurus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.
 1 (bases 1 to 484)
 REFERENCE
 AUTHORS
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keeler, J.W.
 TITLE
 JOURNAL
 COMMENT
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR primers
 FORWARD: AGGAACACAGCTATGACCAT
 BACKWARD: GTTITCCAGTCACGACG
 Plate: 104 row: K column: 22
 Seq primer: ATTTAGGTGACATATAG.
 Location/Qualifiers
 FEATURES
 source
 1..484
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 3BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
 BASE COUNT 101 a 146 c 131 g 106 t
 ORIGIN
 Query Match 18.7%; Score 94.6; DB 13; Length 484;
 Best Local Similarity 58.2%; Pred. No. 2.6e-13;
 Matches 188; Conservative 0; Mismatches 129; Indels 6; Gaps 1;
 QY 40 GTTCTGTCCACAGCTCACGGCAGCTGCTCAACCTGAAGGCCATGTTGGAGGCCGTCACA 99
 Db 62 GGTGTGGCTCCAGCGGAGCGGACATCTGTGACCTGAACAGATGGTCAGACAAGTCACG 121
 QY 100 GGGAGGAGCGCATCTCTCTCTGTTGGGTACGGTTGCTACTGTGGCTGGGGGCGCT 159
 Db 122 GGAAGATCCCATCTTCTTCTTATTCACATATGCTGTACTGCAGAAAAGGTGGCAA 181
 QY 160 GGCCAGCCCAAGGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
 Db 182 GGCCAAACCCAGAGATGCCACAGAGGTCGTCGCGGTGACCATGACTGCTGTACCGTCAC 241
 QY 220 CTCTTTGACCAAGGCTGTCAACCCCTATGTGGACCATATGATCATACCATCGAACAAC 279
 Db 242 CTGAATCTGACAACTGTGACATCAGCTTCGACCATATGACTACACCTT-----TTTC 295
 QY 280 ACTGAGATAGTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 339
 Db 296 CAGGGGAAATCCAGTGTTCACCAAGGGGAGCTGGTGTGAGCAGCAGCTGTGGCCCTGT 355
 QY 340 GACAAGACATGTTCTGTGCT 362
 Db 356 GACAAGACGTTGGCTTCTGCT 378
 RESULT 10
 BF781906
 LOCUS
 DEFINITION 602105856F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4234596 5', mRNA sequence.

QY	331	TGCATGTGTGACAAGA	346
Db	374	TGGCCCTGTGACAAGA	389
III IIIIIIIII			
RESULT	13		
BM363855			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
BM363855			
BS320033000E8			
Subtracted Lewin Cattle Spleen			
CDNA clone			
EST.			
GI:18107224			
cow.			
Bos taurus			
Eukaryota;			
Metazoa; Chordata;			
Cranialia; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
Bovidae; Bovinae; Bos.			
(Bases 1 to 558)			
Lewin,H.A., Soares,M.B., Pardinas,J., Liu,L. and Larson,J.H.			
Unpublished (2002)			
Contact: Lewin, H. A.			
W. M. Keck Center for Comparative and Functional Genomics			
University of Illinois at Urbana-Champaign			
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL			
61801, USA			
Tel: 217 333 5998			
Fax: 217 244 5617			
Email: h-lewineuiuc.edu			
Funding for Cattle EST sequencing was provided by the USDA National			
Research Initiative, Project No. 98-35205-6644, and a grant from			
the Japanese Ministry of Agriculture Fisheries and Forestry to			
H.A. Lewin and J.E.Womack. Base-calling/Quality scores: PHRED form			
Washington University Genome Center. Vector-trimming: Cross_Match			
from Washington University Genome Center PHRAP suite. This sequence			
is vector free and at least 200bp in length.			
Insert Length: 558 Std Error: 0.00			
Plate: BS320033000 row: E column: 8			
Seq primer: CGCCAAGTCGAATAATCAACC			
High quality sequence stop: 558.			
Location/Qualifiers			
1..558			
/organism="Bos taurus"			
/strain="Angus"			
/db_xref="taxon:9913"			
/clone="BS320033000E8"			
/clone.lib="Subtracted Lewin Cattle Spleen"			
/sex="female"			
/dev_stage="Adult"			
/note="Organ: Spleen; Vector: pBluescript SK(+/-); Site:1: EcoRI; Site_2: XhoI; This BS cDNA library was generated by subtraction of the original non-normalized bovine spleen library with 16,800 previously sequenced clones from a bovine placenta cDNA library. The original library was constructed as described by Band et al (2000), Genome Research 10(9): 1359 -1368."			
BASE COUNT	127 a	167 c	149 g
ORIGIN			
Query Match	17.6%	Score 89.2;	DB 13;
Best Local Similarity	58.1%;	Pred. No. 6.1e-12;	
Matches	179;	Conservative	0; Mismatches 123; Indels 6; Gaps 1
QY	55	CACGGCAGCGTGTCAACCTGAAGCCGTGGTAGGCCGTACACGAGGAGCGCCATC	114
Db	2	CACGAGGACATACTGGACCTGAACGAGATGGTGACACAGTGCAGGGGAAGATCCCATC	61
QY	115	CTGTCCTTCGTGGCGTACGGTTCTACTCTGGGCTGGGGCGCGTGCACGAGGAT	174
Db	62	TTCTTCTATTACACATATGCTGTACTGCAGAAAAAGGTGGCCCAAGCCAAACCCAGAGAT	121
QY	175	GAGGTGGACATGGTGTCACAGCCACGACTGCTGTCTACCAGGAACCTCTTTTGACCAAGGC	234

RESULT 12	AW659630	392 bp	mRNA	linear	EST 25-APR-2001
LOCUS	97101 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.				
DEFINITION	AW659630				
ACCESSION	AW659630.1	GI:7425457			
VERSION	EST.				
KEYWORDS	COW.				
SOURCE	Bos taurus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 392)				
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrnerkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perle, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904 e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR Primers FORWARD: AGGAACACGATGACCAT BACKWARD: GTTTCCCGCATCAGCAGC Plate: 68 row: M column: 6 Seq primer: ATTGAGTGACACTATAG. Location/Qualifiers 1..392 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 1BOV" /tissue_type="pooled" /lab_host="DH10B" /note="vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary." 102 a 103 c 109 g 78 t				
FEATURES	source				
BASE COUNT	102 a 103 c 109 g 78 t				
ORIGIN	Query Match 17.6%; Score 89.2; DB 10; Length 392; Best Local Similarity 57.6%; Pred. No. 5.4e-12; Matches 182; Conservative 0; Mismatches 128; Indels 6; Gaps 1;				
QY	31 GTGCGCGGTTCTGTCACAGCTCAGCGCAGCCGCTCAACTGAAGGCCATGCTGGAG 90				
DB	80 GCTTCAGGTTGTGGCTGCTCAGCCGAGGCTGCATCTGACACTGACAGAGATGCTCAGA 139				
QY	91 GCGGTTCACAGGAGGAGGCCCATCTCTCTTCGTTGGGCTACGGTTGCTACTGTGGGCTG 150				
DB	140 CAAGTCAGGGGAAGATCCCCATCTTCTTCTATTCACACTATGGCTGTGTTCAGCAAAA 199				
QY	151 GGGGGCGTGGCCAGCCCAAGATGAGGTGGACTGGTGTGCTGCCAGCCGACGACTGCTGC 210				
DB	200 GGTGCGCAAGGCCCAACCCGGAGTGCCACAGACAGTGTGCTGCCGAGAATCATGCTGCTGC 259				
QY	211 TACCAGGAACCTCTTTGACCAAGGCTGTCCACCCTATGTGGACCACTATGATCATCACCATC 270				
DB	260 TACCGTCACTGAAATCTGCAACTGTGCATCAGCTTCGACCACTATGACTACACCTT- 318				
QY	271 GAGAACAACTGATAGTATGCTGCACTGACCTCAACACAGACAGAGTGTCAAGACGACAGA 330				
DB	319 -----TTTCCAGGGGACATCCAGTGTTCACCAAGGGGAGCTGGTGTGAGCAGCAGCTG 373				

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:27 ; Search time 36 Seconds
(without alignments)
621.836 Million cell updates/sec

Title: US-09-975-456B-2
Perfect score: 957
Sequence: 1 MKKFFTVAILAGSVLSTAHG.....EPPEEVTCSHQSPAPP 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

Database :
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Query			ID	Description
			Match	Length	DB		
1	957	100.0	211	23	AB080202	Human lipid metabo	
2	353	36.9	145	22	AAU09096	Novel human protei	
3	352	36.8	145	21	AA012537	Human secretory ph	
4	352	36.8	145	21	AA030637	Human phospholipas	
5	352	36.8	145	22	AA011924	Human CG95 (or C87	
6	352	36.8	145	22	AA024100	Human EST encoded	
7	352	36.8	150	22	AA025827	Human protein sequ	
8	344.5	36.0	144	21	AA011994	Mouse secreted pho	
9	344.5	36.0	144	21	AA012536	Mouse secretory ph	
10	313.5	32.8	142	21	AA012810	Mouse secretory tv	

ALIGNMENTS

RESULT 1	
ABB08202	
ID	ABB08202 standard; Protein; 211 AA.
XX	
XX	ABB08202;
XX	
XX	
DT	04-MAR-2002 (first entry)
XX	
DE	Human lipid metabolism enzyme-2 (LME-2).
XX	
KW	Human; LME-2; lipid metabolism enzyme-2;
KW	immunosuppressive; anti-inflammatory; cas-
KW	enzyme therapy; cancer; neurological dis-
KW	inflammatory disorder; cardiovascular di-
XX	
OS	Homo sapiens.
XX	
XX	WO200185956-A2.
XX	
PD	15-NOV-2001.
XX	
PF	11-MAY-2001; 2001WO-US15210.
XX	
PR	11-MAY-2000; 2000US-203511P.
XX	
PR	25-MAY-2000; 2000US-207903P.
XX	
PR	07-JUN-2000; 2000US-210150P.
XX	
PR	23-JUN-2000; 2000US-213392P.
XX	
PA	(INCY) INCYTE GENOMICS INC.

PI Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;

Human; LME-2; lipid metabolism enzyme-2; cytostatic; neuroprotective; immunosuppressive; anti-inflammatory; cardiovascular; gene therapy; enzyme therapy; cancer; neurological disorder; autoimmune disorder; inflammatory disorder; cardiovascular disorder.

SECRET NO: 2 of the publication

	Table R
--	---------


```

XX SQ Sequence 145 AA;
Query Match 36.9%; Score 353; DB 22; Length 145;
Best Local Similarity 45.5%; Pred. No. 3.7e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA-----HGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLCGLVWAGVPIPTGGILNLKMKVKQVTGKMPILSWPYGCHGCGLGGRGQPKDATDW 62

QY 63 CCHAHCCVQELFDQCHPYVDHYDHTIENNTFIVCSDLNKTECDKQTCMCDKNNVLCLM 122
   || ||||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 63 CCQTHDCCYDHLTKQCGSIYKDYRYNFSQ- NIHCSD- KGSWCQQLCACDKEVAFCLK 120

QY 123 N--QTYREEYRGFLNVYCGPTPNC 145
   ||:: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 3
AAB12537
ID AAB12537 standard; Protein; 145 AA.
AC AAB12537;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human secretory phospholipase A2 protein sequence SEQ ID NO:27.
XX
KW Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW antibacterial; immunosuppressive; tranquilizer; vulnerary;
KW antirheumatic; antiarthritic; septic shock; trauma; pancreatitis;
KW allergic rhinitis; chronic rheumatoid arthritis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= signal
FT Protein 21..145
FT /label= PLA2
XX
PN WO200034486-A1.
XX
PD 15-JUN-2000.
XX
PF 07-DEC-1999; 99WO-JP06844.
XX
PR 09-DEC-1998; 98JP-0349608.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Ishizaki J, Suzuki N, Hanasaki K;
DR WPI; 2000-423429/36.
DR N-PSDB; AAA60878.
XX
PT Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT diagnosis and treatment of secretory PLA2-associated diseases e.g.
PT septic shock, trauma, pancreatitis, allergic rhinitis and chronic
PT rheumatoid arthritis.
XX
PS Claim 1; Page 41; 45pp; Japanese.
XX
CC The present invention describes human secretory phospholipase A2 (PLA2).
CC PLA2 has antiallergic, antiinflammatory, antibacterial, tranquilizer,
CC immunosuppressive, vulnerary, antirheumatic and antiarthritic
CC activities. Human secretory phospholipase A2 (PLA2), the gene encoding
CC it and antibodies against it are useful for the diagnosis and treatment
CC of secretory PLA2-associated diseases e.g. septic shock, trauma,
CC pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC present sequence represents human PLA2.

```

```

XX SQ Sequence 145 AA;
Query Match 36.8%; Score 352; DB 21; Length 145;
Best Local Similarity 45.5%; Pred. No. 4.6e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 7 VAILAGSVLSTA-----HGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDW 62
   :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 3 LALLCGLVWAGVPIPTGGILNLKMKVKQVTGKMPILSWPYGCHGCGLGGRGQPKDATDW 62

QY 63 CCHAHCCVQELFDQCHPYVDHYDHTIENNTFIVCSDLNKTECDKQTCMCDKNNVLCLM 122
   || ||||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 63 CCQTHDCCYDHLTKQCGSIYKDYRYNFSQ- NIHCSD- KGSWCQQLCACDKEVAFCLK 120

QY 123 N--QTYREEYRGFLNVYCGPTPNC 145
   ||:: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 4
AAB03627
ID AAB03627 standard; protein; 145 AA.
XX
AC AAB03627;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human phospholipase 1 HPPL1.
XX
KW Human; phospholipase 1; HPPL1; cancer; autoimmune disorder;
KW inflammatory disorder; reproductive disorder; infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= putative_signal_peptide
FT Peptide 1..16
FT /label= putative_signal_peptide
FT Protein 17..145
FT /label= putative_mature_HPPL1
FT Active-site 21..145
FT /label= phospholipase_A2_active_site_signature
FT Protein 22..145
FT /label= putative_mature_HPPL1
FT Modified-site 33
FT /label= potential_phosphorylation_site
FT Region 44..92
FT /label= active_site_histidine_region
FT Region 88..140
FT /label= active_site_aspartic_acid_region
FT Modified-site 89
FT /label= potential_glycosylation_site
FT Modified-site 98
FT /label= potential_phosphorylation_site
FT Modified-site 102
FT /label= potential_phosphorylation_site
XX
PN WO200024911-A2.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US25021.
XX
PR 27-OCT-1998; 98US-0181317.
PR 21-JAN-1999; 99US-0234726.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;
PI Azimzai Y, Lal P, Lu DAM;
XX

```


XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX Homo sapiens.
 OS WO200154477-A2.
 PN 02-AUG-2001.
 PD 25-JAN-2001; 2001WO-US03687.
 XX 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX WPI: 2001-476164/51.
 DR N-PSDB; AAH98759.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 PS Claim 20; Page 1102; 1275pp; English.
 XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX Sequence 145 AA;
 SQ Query Match 36.8%; Score 352; DB 22; Length 145;
 Best Local Similarity 45.5%; Pred. No. 4.6e-25;
 Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;
 QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYCYCGLGGRGQPKDEVDW 62
 DB 3 LALLGLVVMAGVPIQGGILNLKNKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDADTW 62
 QY 63 CCHAHDCCYQELFQGGCHPYVDHYDHTIENNTIENVCSDLNKTCDKQTCMDKNMVLCLM 122
 DB 63 CCQTHDCCYDHLKQTGGGKDYRYNFSQG-NIHCSG-KGSWCEQQLCACDKEVAFCLK 120
 QY 123 N--QTYREYRGFLNVYCOGPTNC 145
 DB 121 RNLDTYQKRLRFYWRPHCRGQTGCG 145
 RESULT 7
 AAM25827
 ID AAM25827 standard; Protein; 150 AA.
 XX AAM25827;
 AC AAM25827;
 XX 16-OCT-2001 (first entry)
 DT Human protein sequence SEQ ID NO:1342.
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;

KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neoprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; aschma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.
 XX Homo sapiens.
 OS WO200153455-A2.
 PN 26-JUL-2001.
 PD 22-DEC-2000; 2000WO-US35017.
 XX 23-DEC-1999; 98US-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI: 2001-457603/49.
 DR N-PSDB; AAH99768.
 XX Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 PS Claim 20; Page 278; 1217pp; English.
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antinflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianemic; antiaggregant; haemostatic; vulnery;
 CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX Sequence 150 AA;
 SQ Query Match 36.8%; Score 352; DB 22; Length 150;
 Best Local Similarity 45.5%; Pred. No. 4.8e-25;
 Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;
 QY 7 VAILAGSVLSTA----HGSLNLKAMVEAVTGRSAILSFVGYCYCGLGGRGQPKDEVDW 62
 DB 8 LALLGLVVMAGVPIQGGILNLKNKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDADTW 67
 QY 63 CCHAHDCCYQELFQGGCHPYVDHYDHTIENNTIENVCSDLNKTCDKQTCMDKNMVLCLM 122
 DB 68 CCQTHDCCYDHLKQTGGGKDYRYNFSQG-NIHCSG-KGSWCEQQLCACDKEVAFCLK 125

121 NLD SYN KRL RYY WRP RCKGKTPAC 144

[illegible]

•

[illegible]

Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic; glycerophospholipids; non-pancreatic.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..20 /label= signal
 Peptide 21..39 /note= "Claim 12"
 Peptide 22..37 /note= "Claim 14"
 Region 1..14 /label= exon_1
 Region 15..62 /label= exon_2
 Region 63..98 /label= exon_3
 Region 99..124 /label= exon_4
 Region 44..56 /note= "calcium binding loop"
 Binding-site 68 /note= "calcium binding"
 Binding-site 67
 Active-site 71
 Active-site 86
 Active-site 111
 WO8909818-A.
 19-OCT-1989.

11-APR-1989; 89WO-US01418.

15-APR-1988; 88US-0181893.

(BIOJ) BIOGEN INC.

Kramer RM, Pepinsky RB, Hession C;

WPI; 1989-324225/44.

N-PSDB; AAN91825, AAN97209.

Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation of diseases.

Claim 44; Fig 12; 84pp; English.

The protein sequence was deduced from a DNA sequence obt'd. from a genomic DNA library which was prep'd. from a mutant fibroblast cell line which contains 5 copies of the X chromosome (GM5009). The signal sequence is thought to be incomplete at the N-terminal since no promoter-like sequences are found in the DNA within 100 nucleotides 5' of this region. The deduced N-terminal sequence of the mature protein confirmed results obt'd. by direct sequencing of the purified protein. This sequence represents an amphiphilic alpha-helix typical of PLA₂ moieties. It has highly conserved lipophilic residues [e.g. Leu (22), Phe (25), and Ile (29)] and there is a cluster of basic amino acids [e.g. Arg (27), Lys (30) and Lys (35)] which is believed to be an important determinant in the interaction of PLA₂. There is a characteristic stretch of residues which comprises part of the calcium binding loop: Tyr(44)-Gly-Cys-X-Cys-Gly-X-Gly-X-X-Pro(56) and Asp(68). The conserved residues which constitute the active site (see features) are also present, and the protein exhibits the placement of half-cysteine residues typical of a Gp II PLA₂, having a Cys residue at position 70 and a half cysteine at the C-terminal. (The consensus sequence was determined from a comparison of PUA₂s from bovine pancreas and C. atrox venom.

Sequence 144 AA;

Query Match 31.6%; Score 302.5; DB 10; Length 144;
 Best Local Similarity 38.8%; Pred. No. 1.8e-20;
 Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

QY 1 MKKFFTVAILAGSVLSTAHGSLNKLKAMVEAVTGRSAILSFVGYCYCGLGGRGPKDEV 60
 DB 1 MKTLLLVAVIMIFGLQAHGNLVNFRMIKLTGKRAALSFGYCHGCGVGRGSPKDAT 60
 QY 61 DMCCHADCCYQBLFDQCHPYVDHYDHTIENNTETVCSLDLNTKTECDKQTCMCDKNWVLC 120
 DB 61 DRCCVTHDCCYKRLKRGCGTFLSYKFS-NSGSRITCA--KODSCRSOLCECDKAAATC 117
 QY 121 LMNQ--TYREYRGFLNVCYCGQPTPNC 145
 DB 118 FARNKTTYNNKYQYYSNKHCRGSTPRC 144

RESULT 15

AAR25416

ID AAR25416 standard; Protein; 144 AA.

XX AAR25416;

DT 06-JAN-1993 (first entry)

XX PLA2.

Human growth hormone; granulocyte-colony stimulating factor; G-CSF;
 phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;
 erythroid cells; cDNA library.

OS Synthetic.

XX GB2251622-A.

XX 15-JUL-1992.

PF 19-DEC-1991; 91GB-0026984.

PR 21-DEC-1990; 90GB-0027917.

XX (ICIL) IMPERIAL CHEM IND PLC.

PI Antoniou M, Gooding C, Grosveld FG, Hollis M, Needham MRC;
 XX WPI; 1992-236158/29.

DR N-PSDB; AAQ26372.

XX Expression vectors for use in mammalian cells - contain dominant
 control region derived from beta-globin gene

XX Disclosure; Fig 11; 77pp; English.

This sequence is encoded by the phospholipase A2 (PLA₂) cDNA. The
 cDNA was amplified using the primer sequences given in AAQ26370-1 by
 PCR from a human lung cDNA library. The cDNA sequence was used in
 the construction of an expression vector which further comprised a
 promoter and a dominant control region. This vector was used in an
 expression system comprising a mammalian cell transformed with the
 vector. This expression system could be used to prepare
 pharmacologically useful polypeptides eg. human growth hormone (HGH),
 granulocyte-colony stimulating factor (G-CSF) and PLA₂, and for gene
 therapy. The mammalian host comprises erythroid cells and a
 heterologous promoter.

XX Sequence 144 AA;

Query Match 31.6%; Score 302.5; DB 13; Length 144;

Best Local Similarity 38.8%; Pred. No. 1.8e-20;

Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

QY 1 MKKFFTVAILAGSVLSTAHGSLNKLKAMVEAVTGRSAILSFVGYCYCGLGGRGPKDEV 60
 DB 1 MKTLLLVAVIMIFGLQAHGNLVNFRMIKLTGKRAALSFGYCHGCGVGRGSPKDAT 60

Mon Feb 10 11:36:14 2003

Db 1 MKTLLLVIMIFGLLOAHGNLVNFHRMIKLTGTGKEAALSYGFYCHCGVGRGSPKDAT 60
Qy 61 DWCCCHADCCYQELFDQCHPYVDHYDHTIENNTEIVGSDLNKTECDKQTCMCKNMVLC 120
Db 61 DRCCVTHDCCYKLEKRGCGTKFELSYKFS-NSGSRITCA--KQDSRSQLCECDKAAATC 117
Qy 121 LMNQ--TYREEYRGFLNVYCOGFTPNC 145
Db 118 FARNKTYNKKOYYSNKHCRGSTPRC 144

Search completed: February 10, 2003, 10:36:32
Job time : 38 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:31 : Search time 15 seconds
(without alignments)
329.537 Million cell updates/sec

Title: US-09-975-456b-2
Perfect score: 957
Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	302.5	31.6	144	1	US-08-186-895-10
2	302.5	31.6	144	2	US-08-888-497-37
3	302.5	31.6	144	4	US-09-362-230-37
4	302.5	31.6	144	5	PCT-US94-07926-37
5	294.5	30.8	146	3	US-08-966-317-4
6	294.5	30.8	146	4	US-09-489-770-4
7	288.5	30.1	146	2	US-08-888-497-35
8	288.5	30.1	146	4	US-09-362-230-35
9	288.5	30.1	146	5	PCT-US94-07926-35
10	283	29.6	146	3	US-08-966-317-3
11	283	29.6	146	4	US-09-489-770-3
12	278	29.0	125	2	US-08-888-497-42
13	278	29.0	125	4	PCT-US94-07926-42
14	278	29.0	125	5	US-08-170-360-4
15	275.5	28.8	124	1	US-08-888-497-39
16	275.5	28.8	124	2	US-09-362-230-39
17	275.5	28.8	124	4	PCT-US94-07926-39
18	275.5	28.8	124	5	US-08-888-497-32
19	275.5	28.8	138	2	US-09-362-230-32
20	275.5	28.8	138	4	PCT-US94-07926-32
21	268.5	28.1	137	2	US-08-888-497-30
22	268.5	28.1	137	4	PCT-US94-07926-30
23	268.5	28.1	137	5	US-08-966-317-1
24	268.5	28.1	165	3	US-08-888-497-43
25	268.5	28.1	165	4	US-08-888-497-43
26	268.5	28.1	165	5	US-08-888-497-43
27	267	27.9	130	2	US-08-888-497-43

28	267	27.9	130	4	US-09-362-230-43	Sequence 43, Appl
29	267	27.9	130	5	PCT-US94-07926-43	Sequence 43, Appl
30	267	27.9	158	2	US-08-888-497-22	Sequence 22, Appl
31	267	27.9	158	4	US-09-362-230-22	Sequence 22, Appl
32	267	27.9	158	5	PCT-US94-07926-22	Sequence 22, Appl
33	264.5	27.6	118	2	US-08-888-497-40	Sequence 40, Appl
34	264.5	27.6	118	4	US-09-097-094-5	Sequence 5, Appl
35	264.5	27.6	118	5	US-09-362-230-40	Sequence 40, Appl
36	264.5	27.6	118	5	PCT-US94-07926-40	Sequence 40, Appl
37	250	26.1	125	1	US-08-170-360-5	Sequence 5, Appl
38	249.5	26.1	117	2	US-08-888-497-44	Sequence 44, Appl
39	249.5	26.1	117	4	US-09-362-230-44	Sequence 44, Appl
40	249.5	26.1	117	5	PCT-US94-07926-44	Sequence 44, Appl
41	237	24.8	124	1	US-08-170-360-1	Sequence 1, Appl
42	236.5	24.7	122	1	US-07-734-534A-1	Sequence 1, Appl
43	225.5	23.6	146	2	US-08-888-497-34	Sequence 34, Appl
44	225.5	23.6	146	4	US-09-362-230-34	Sequence 34, Appl
45	225.5	23.6	146	5	PCT-US94-07926-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosfeld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-186-895-10

Query Match 31.6%; Score 302.5; DB 1; Length 144;
Best Local Similarity 38.8%; Pred. No. 8.9e-22;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

```

Db      61 DRCCVTHDCCYRLEKRCGGTKFLSYKFS--NSGSRITCA--KQDSCRSQLCECDKAAATC 117
      QY      121 LMNQ--TYREYRGFLNVCYCGPTPC 145
      DB      118 FARNKTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 3
US-09-362-230-37
; Sequence 37, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Mischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broadway
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-362-230-37

Query Match 31.6%; Score 302.5; DB 4; Length 144;
Best Local Similarity 38.8%; Pred. No. 8.9e-22;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

QY      1 MKKFTTVAILAGSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYGCYGLGGRGOPKDEV 60
      DB      1 MKTLLLAIVIMFGLLOAGNLVNFHRMILKLTGKEALSYFGYCHCGVGGSGPKDAT 60
      QY      61 DWCHHAHDCCYQELFDGCGHPYVDHYDHTIENNTETVCSDLNKTCDKQTCMCDKNWLC 120
      DB      61 DRCCVTHDCCYRLEKRCGGTKFLSYKFS--NSGSRITCA--KQDSCRSQLCECDKAAATC 117
      QY      121 LMNQ--TYREYRGFLNVCYCGPTPC 145
      DB      118 FARNKTTYNKKYQYYSNKHCRGSTPRC 144

```

DB 1 MKTLLAVIMFGLLQAHGLNLFNFKHKLITLTKGKAALSLGFIGCGYGVGNQKRNK 60

QY 61 DWCHAHDCQYQELFDGCGHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNNWLC 120

DB 61 DECCVTHDCCYKRLKRGCGTKFLSYKFS-NSGSRITCA--KQDSCRSQLCECDKAATC 117

QY 121 LMNQ--TYREYRGFLNVYCOGTPNC 145

DB 118 FARNKTTYNKYQYYSNKHKRGSTPRC 144

RESULT 4
PCT-US94-07926-37
; Sequence 37, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07926-37

Query Match 31.6%; Score 302.5; DB 5; Length 144;
Best Local Similarity 38.8%; Pred. No. 8.9e-22;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;
QY 1 MKKFFTVAILAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGCGLGGRGPKDEV 60
Db 1 MKTLLLLAVIMIFGLLQAHGNLVNFRMIKLTGKEAALSFGYCYGCGVGGRGSPKDAT 60
QY 61 DMCHAHDCCYQLFDGCHPYVDHYDHTIENNTIIVCSDLNKTEDKQTCMCDKNMVLIC 120
Db 61 DRCVTHDCCYKRLKRGCGTKFLSKFS-NSGSRITCA--KQDSCRQLCECDKAAATC 117
QY 121 LMNQ--TYREYRGFLNVCYCGPTPNC 145
Db 118 FARNKTTYNNKKYQYYSNKHCRGSTPRC 144

RESULT 5
US-08-966-317-4
; Sequence 4, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga

; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 204319
US-08-966-317-4

Query Match 30.8%; Score 294.5; DB 3; Length 146;
Best Local Similarity 42.3%; Pred. No. 5.2e-21;
Matches 60; Conservative 20; Mismatches 55; Indels 7; Gaps 5;
QY 7 VAILA-GSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGCGLGGRGPKDEVDMCH 65
Db 9 VWIMAFGSI--QVQSLLEFGQWILFKTKRADVSVGYCYGCGVGGRGSPKDATDMCCV 66
QY 66 AHDCCYQLFDGCHPYVDHYDHTIENNTIIVCSDLNKTEDKQTCMCDKNMVLICM--N 123
Db 67 THDCCYNRLKRCGCKGTFYKFSYRGG-OISCS-TNODSCRKQLCQCDKAAAECEFARNK 124
QY 124 QTYREYRGFLNVCYCGPTPNC 145
Db 125 KYSLSKYQVFLNKFCKGKTPSC 146

RESULT 6
US-09-489-770-4
; Sequence 4, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.

Mon Feb 10 11:36:15 2003

```
;
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
;
; US-09-489-770-4
;
; Query Match 30.8%; Score 294.5; DB 4; Length 146;
; Best Local Similarity 42.3%; Pred. No. 5.2e-21;
; Matches 60; Conservative 20; Mismatches 55; Indels 7; Gaps 5;
;
; QY 7 VAILA-GSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCC 65
; Db 9 VVIMAFGSI--QVQGSLLFEGQMILFKTKRADYSYGFYGCYCHGCGVGRGSPKDATDMCCV 66
;
; QY 66 AHDCYQELFDQCHPYVDHYDHTIENNTIIVCSLDINKTECDKQTCMCKNNVLCLM--N 123
; Db 67 THDCYNNRLEKRGCGTKFLTYKFSYRGQ-QISCS-TNQDSCKRQLCQCDKAAAECPARNK 124
;
; QY 124 QTYREYRCFLNVCQGPPTNC 145
; Db 125 KSYSLKYQFYLNKFCGKPTPC 146
;
; RESULT 7
; US-08-888-497-35
; Sequence 35, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-888-497-35
;
; Query Match 30.1%; Score 288.5; DB 2; Length 146;
; Best Local Similarity 41.5%; Pred. No. 2e-20;
; Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;
;
; QY 7 VAILA-GSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCC 65
; Db 9 VVIMAFGSI--QVQGSLLFEGQMILFKTKRADYSYGFYGCYCHGCGVGRGSPKDATDMCCV 66
;
; QY 66 AHDCYQELFDQCHPYVDHYDHTIENNTIIVCSLDINKTECDKQTCMCKNNVLCLM--N 123
; Db 67 THDCYNNRLEKRGCGTKFLTYKFSYRGQ-QISCS-TNQDSCKRQLCQCDKAAAECPARNK 124
;
; QY 124 QTYREYRCFLNVCQGPPTNC 145
; Db 125 KSYSLKYQFYLNKFCGKPTPC 146
;
; RESULT 8
; US-09-362-230-35
; Sequence 35, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35
;
; Query Match 30.1%; Score 288.5; DB 4; Length 146;
; Best Local Similarity 41.5%; Pred. No. 2e-20;
; Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;
;
; QY 7 VAILA-GSVLSTAHGSLNLLKAMVEAVTGRSAILSEFVGYCGYGLGGRGQPKDEVDWCCH 65
; DB 9 VVIMAFGSI--QVQGSLLLEFGQMILFKTKRADVSFYGCHGCGVGRGSPKDATDWCVCV 66
;
; QY 66 AHDCCYQELFDQGCCHPYVDHYDHTIENNTETVCSDLNKTCDKQTCMCDKNMVLCLM--N 123
; DB 67 THDCCYNRLKRGCGTKFYTKFSYRGQ-QISCS-TNODSCRKQLCQCDKAAAEFCFARK 124
;
; QY 124 QTYREYRGFLNVYCGGTPNC 145
; DB 125 KSYSLAYQYPNKFCKGKTPSC 146
;
; RESULT 9
; PCT-US94-07926-35
; Sequence 35, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhammer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35
;
; Query Match 30.1%; Score 288.5; DB 5; Length 146;
; Best Local Similarity 41.5%; Pred. No. 2e-20;
; Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;
;
; QY 7 VAILA-GSVLSTAHGSLNLLKAMVEAVTGRSAILSEFVGYCGYGLGGRGQPKDEVDWCCH 65
; DB 9 VVIMAFGSI--QVQGSLLLEFGQMILFKTKRADVSFYGCHGCGVGRGSPKDATDWCVCV 66
;
; QY 66 AHDCCYQELFDQGCCHPYVDHYDHTIENNTETVCSDLNKTCDKQTCMCDKNMVLCLM--N 123
; DB 67 THDCCYNRLKRGCGTKFYTKFSYRGQ-QISCS-TNODSCRKQLCQCDKAAAEFCFARK 124
;
; QY 124 QTYREYRGFLNVYCGGTPNC 145
; DB 125 KSYSLAYQYPNKFCKGKTPSC 146
;
; RESULT 10
; US-08-966-317-3
; Sequence 3, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0535
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
```

	9	ILAGSVLS-----TAHGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGPKDEVWCC	64
QY		: :::	:
Db	6	LLAASIMAFSGISQVOGNIAQFAGEMIRLTKTGRAELSYAFYCHGCGKGSPKDTRCC	65
		: :::	:
QY	65	HAHDCCYOELFDQGCHPYVDHYDHTIENNTIEIVCSDLNKTCDKOTCMCKNMVLCLM--	122
		: :::	:
Db	66	VTHDCCYKLESGCGTKLKLYKHSHQGG-QITCS-ANQNSCQKRLCOCDRAAAECFARN	123
		: :::	:
QY	123	NOTYREERYRGLNVYCQGPPTNC	145
		: :::	:
Db	124	KKTYSLKQFYFPNMFCKGKKPKC	146
		: :::	:
RESULT 12			
US-08-888-497-42			
; Sequence 42, Application US/08888497			
; Patent No. 5972677			
; GENERAL INFORMATION:			
; APPLICANT: Tischfield, Jay A.			
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide			
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences			
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide			
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites			
; NUMBER OF SEQUENCES: 44			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &			
; ADDRESS: Russell PA			
; STREET: 200 East Broward Boulevard			
; CITY: Fort Lauderdale			
; STATE: FL			
; COUNTRY: USA			
; ZIP: 33301			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/888,497			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/651,405			
; FILING DATE:			
; APPLICATION NUMBER: US 08/097,354			
; FILING DATE: 26-JUL-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Manso, Peter J.			
; REGISTRATION NUMBER: 32,264			
; REFERENCE/DOCKET NUMBER: IN21044-5			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 305-527-2498			
; TELEFAX: 305-764-4996			
; INFORMATION FOR SEQ ID NO: 42:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 125 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-888-497-42			
Query Match 29.0%; Score 278; DB 2; Length 125;			
Best Local Similarity 41.7%; Pred. No. 1.7e-13;			
Matches 53; Conservative 18; Mismatches 52; Indels 4; Gaps 3;			
QY	21	SLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGPKDEVWCCAHDCCYOELFDQGC	80
		: :::	:
Db	1	SLLFGOMLFKTKRADVSYGFGYCHGCGVGGRGSPKDTRCCVTHDCYNRLEKRCG	60
		: :::	:
QY	81	PVVDHYDHTIENNTIEIVCSDLNKTCDKOTCMCKNMVLCLM--NOTYREERYRGLNVYC	138
		: :::	:
LIBRARY: GenBank			
CLONE: 984837			
US-08-966-317-3			
Query Match 29.6%; Score 283; DB 3; Length 146;			
Best Local Similarity 37.1%; Pred. No. 6.6e-20;			
Matches 53; Conservative 26; Mismatches 56; Indels 8; Gaps 4;			
QY	9	ILAGSVLS-----TAHGSLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGPKDEVWCC	64
		: :::	:
Db	6	LLAASIMAFSGISQVOGNIAQFAGEMIRLTKTGRAELSYAFYCHGCGKGSPKDTRCC	65
		: :::	:
QY	65	HAHDCCYOELFDQGCHPYVDHYDHTIENNTIEIVCSDLNKTCDKOTCMCKNMVLCLM--	122
		: :::	:
Db	66	VTHDCCYKLESGCGTKLKLYKHSHQGG-QITCS-ANQNSCQKRLCOCDRAAAECFARN	123
		: :::	:
QY	123	NOTYREERYRGLNVYCQGPPTNC	145
		: :::	:
Db	124	KKTYSLKQFYFPNMFCKGKKPKC	146
		: :::	:
RESULT 11			
US-09-489-770-3			
; Sequence 3, Application US/09489770			
; Patent No. 6399301			
; GENERAL INFORMATION:			
; APPLICANT: Hawkins, Phillip R.			
; APPLICANT: Bandman, Olga			
; APPLICANT: Gugler, Karl J.			
; APPLICANT: Shah, Purvi			
; APPLICANT: Corley, Neil C.			
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN			
; NUMBER OF SEQUENCES: 4			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Incyte Pharmaceuticals, Inc.			
; STREET: 3174 Porter Dr.			
; CITY: Palo Alto			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 94304			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/489,770			
; FILING DATE:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/966,317			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Billings, Lucy J.			
; REGISTRATION NUMBER: 36,749			
; REFERENCE/DOCKET NUMBER: PF-0403 US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 650-855-0555			
; TELEFAX: 650-845-4166			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 146 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; IMMEDIATE SOURCE:			
; LIBRARY: GenBank			
; CLONE: 984837			
US-09-489-770-3			
Query Match 29.6%; Score 283; DB 4; Length 146;			
Best Local Similarity 37.1%; Pred. No. 6.6e-20;			
Matches 53; Conservative 26; Mismatches 56; Indels 8; Gaps 4;			

us-09-975-456b-2.ra

Mon Feb 10 11:36:15 2003

```

;
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170.360
; FILING DATE: 03-MAR-1994
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU92/00333
; FILING DATE: 06-JUL-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 7058
; FILING DATE: 04-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-104A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
;
; US-08-170-360-4

```

```

Query Match      28.8%; Score 275.5; DB 1; Length 124;
Best Local Similarity 39.4%; Pred. No. 2.8e-19;
Matches 50; Conservative 21; Mismatches 51; Indels 5; Gaps 3;

Qy 21 SLLNLKAMVEAVTGRSAILSFVGYGCGYGLGGRGQPKDEVDWCCHADCCYQELFDQGGH 80
   :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1 NLVNFHRMIKLTGKEAALSIFYGCHGCGVGGGSPKDATDRCCVTHDCCYKRLEKRGCG 60

Qy 81 PYVDHYDHTIENTEIVCSDLNTECDKOTCMCDKNMVLGMNQ--TYREYRGFLNVYC 138
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TKFLSYKFS-NSGSRITCA--KQDSRSQLCECDKAAATCFARNKTYTNKKYQYYSNKH 117

Qy 139 QGPTPNC 145
   :|||
Db 118 RGSTPRC 124

```

Search completed: February 10, 2003, 10:37:30
Job time : 15 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:37:16 : Search time 11 Seconds
(without alignments)
338.586 Million cell updates/sec

Title: US-09-975-456b-2

Perfect score: 957

Sequence: 1 MKKEFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPPAP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pdb.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pdb.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pdb.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	353	36.9	145	9	US-09-969-384-17
2	352	36.8	145	10	US-09-835-996A-6
3	302.5	31.6	164	10	US-09-925-300-1010
4	294.5	30.8	146	9	US-10-124-591-4
5	283	29.6	146	9	US-10-124-591-3
6	283	29.6	146	10	US-09-993-999-8
7	273.5	28.6	116	9	US-10-028-072-534
8	273.5	28.6	116	9	US-10-121-049-534
9	273.5	28.6	116	9	US-10-123-904-534
10	273.5	28.6	116	9	US-10-140-470-534
11	272.5	28.5	137	10	US-09-993-999-9
12	268.5	28.1	165	9	US-10-124-591-1
13	264.5	27.6	118	9	US-09-987-675-5
14	264.5	27.6	118	10	US-09-987-655-5
15	220.5	23.0	156	10	US-09-925-297-511
16	208.5	21.8	146	10	US-09-993-999-7
17	203.5	21.3	143	10	US-09-993-999-10
18	141.5	14.8	79	10	US-09-925-297-873
19	131	13.7	37	10	US-09-975-374A-14

20	92.5	9.7	604	10	US-09-764-898-211	Sequence 211, App
21	92	9.6	509	10	US-09-781-100-2	Sequence 2, Appl
22	90.5	9.5	1523	9	US-10-174-590-290	Sequence 290, App
23	90.5	9.5	1523	9	US-10-176-758-290	Sequence 290, App
24	90.5	9.5	1523	9	US-10-175-737-290	Sequence 290, App
25	90.5	9.5	1523	9	US-10-173-706-290	Sequence 290, App
26	90.5	9.5	1523	9	US-10-175-738-290	Sequence 290, App
27	90.5	9.5	1523	9	US-10-175-752-290	Sequence 290, App
28	90.5	9.5	1523	9	US-10-176-482-290	Sequence 290, App
29	90.5	9.5	1523	9	US-10-176-757-290	Sequence 290, App
30	90.5	9.5	1523	9	US-10-176-913-290	Sequence 290, App
31	90.5	9.5	1523	9	US-10-180-552-290	Sequence 290, App
32	90.5	9.5	1523	9	US-10-180-557-290	Sequence 290, App
33	90.5	9.5	1523	12	US-10-011-064-2	Sequence 2, Appl
34	90.5	9.5	1523	12	US-10-052-586-290	Sequence 290, App
35	86	8.9	238	10	US-09-925-300-941	Sequence 941, App
36	85	8.9	260	9	US-09-858-546-5	Sequence 2, Appl
37	85	8.9	530	9	US-09-858-546-2	Sequence 84, Appl
38	84.5	8.8	250	10	US-09-739-907-84	Sequence 185, App
39	84.5	8.8	272	10	US-09-739-907-84	Sequence 63, Appl
40	84.5	8.8	467	10	US-09-888-615-63	Sequence 2, Appl
41	84.5	8.8	1239	10	US-09-871-388-2	Sequence 2, Appl
42	84.5	8.8	2444	10	US-09-944-849-2	Sequence 15, Appl
43	83.5	8.7	737	9	US-09-944-413-15	Sequence 15, Appl
44	83.5	8.7	737	9	US-09-944-403-15	Sequence 15, Appl
45	83.5	8.7	737	9	US-09-944-896-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-969-384-17
; Sequence 17, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO55P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-384-17

Query Match 36.9%; Score 353; DB 9; Length 145;
Best Local Similarity 45.5%; Pred No. 14e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY	7	VALLAGSVLSTA----	HGSLNLKAMVEAVTGRSAILSFVGYCYGLGGRGQPKDEVDW	62
Db	3	LALLCGLVVMAGVIPTQGGILNLKMKVKQVTKGMPILSWPYGCHGGLGGRGQPKDATDW	62	
QY	63	CCHAHCCCYQELFDQCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCKNNVLCLM	122	
Db	63	CCOHTDCCDHKLKTCGSIYKDYRYNFSQ--NIHCSD-KGSWCBEQQLACADKEVAFCLK	120	
QY	123	N--QTYREYRGFLNVCYCGQTPNC	145	
Db	121	RNLDTYQKRLRYWRPHCRGQTPGC	145	

RESULT 2

us-09-975-456b-2.rapb

Mon Feb 10 11:36:15 2003

```
US-09-835-996A-6
; Sequence 6, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyan
; APPLICANT: Qian, Xiahong
; APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-835-996A-6

Query Match      36.8%; Score 352; DB 10; Length 145;
Best Local Similarity 45.5%; Pred. No. 1.7e-25;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

Qy  7  VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYCYGGLGGRGPKDEVDW 62
Db  3  LALLCGLVVMAGVIPIOGGILNLKMKVQVIGKMPILSYWPGYCHGGLGGRGPKDADW 62

Qy  63  CCHAHDCCYQELFDQGGHPYVDHYDHTIENNTFIVCSDLNKTECDKQTCMDKNMVLCLM 122
Db  63  CCQTHDCCYDHLKTGGCGIYKYRNFYSQG-NIHCSQD-KGSWCQEQQLCADCKEVAFCLK 120

Qy  123  N--QTYREYRGFLNVYCOGPTPNC 145
Db  121  RMLDTYKRLRFPYRPHCRGOTPGC 145

RESULT 3
US-09-925-300-1010
; Sequence 1010, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1010
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-925-300-1010

Query Match      31.6%; Score 302.5; DB 10; Length 164;
Best Local Similarity 38.8%; Pred. No. 6.7e-21;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;

Qy  1  MKKFTTVAIIAGSVLSTAHSLLNLKAMVEAVTGRSAILSFVGYCYGGLGGRGPKDEV 60
Db  21  MKTLLLAIVIMIFGLQAGNLVNFHRMILTTTKEAALSYGFYGCCHGCGVGGGSPKDAT 80

Qy  61  DWCCCHAHDCCYQELFDQGGHPYVDHYDHTIENNTFIVCSDLNKTECDKQTCMDKNMVLCL 120
Db  81  DRCCVTHDCCYRLEKRCGCTGKFLSYKFS-NSGSRITCA--KQDSQRSQLECDKAAATC 137

Qy  121  LMNQ--TYREYRGFLNVYCOGPTPNC 145
Db  138  FARNKTTYNNKKYQVYSNKHCRGSTPRC 164

RESULT 4
US-10-124-591-4
; Sequence 4, Application US/10124591
; Patent No. US20020177208A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,591
; FILING DATE: 16-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/966,317
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
```

US-10-124-591-4

Query Match 30.8%; Score 294.5; DB 9; Length 146;
 Best Local Similarity 42.3%; Pred. No. 3.2e-20;
 Matches 60; Conservative 20; Mismatches 55; Indels 7; Gaps 5;
 QY 7 VAILA-GSVLSTAHGSLNLKAMVEAVTGRSAILSFVGYCGYGLGGRGQPKDEVDMCC 65
 Db 9 VVIMAFGST--OVQSLLEFGOMILFKTGKRDVSYGYGCGYCGYGLGGRGQPKDEVDMCCV 66
 QY 66 AHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKOTCMCDKNMVLCLM--N 123
 Db 67 THDCYCNLEKRGCGTKELTKFYRGV--QITCS--TNQDSCKQLCCDCAAAAECEAFRNK 124
 QY 124 QTYREYRGFLNVYCGQPTPNC 145
 Db 125 KYSYLYQFYLNKFKCKGKTPSC 146

RESULT 5

US-10-124-591-3
 ; Sequence 3, Application US/10124591
 ; Patent No. US20020177208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hawkins, Phillip R.
 ; Bandman, Olga
 ; Guegler, Karl J.
 ; Shah, Purvi
 ; Corley, Neil C.
 ; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA: US/10/124,591
 ; FILING DATE: 16-Apr-2002
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/489,770
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/966,317
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0403 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 146 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 984837
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 29.6%; Score 283; DB 9; Length 146;
 Best Local Similarity 37.1%; Pred. No. 3.6e-19;
 Matches 53; Conservative 26; Mismatches 56; Indels 8; Gaps 4;

QY 9 ILAGSVLS----TAHGSLLNLKAMVEAVTGRSAILSFVGYCGYGLGGRGQPKDEVDMCC 64
 Db 6 LLAASIMAFGSTQVOGNTAQFGEMIRLTKGRAELSYAFYCGYGLGGRGQPKDEVDMCC 65
 QY 65 HAHDCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKOTCMCDKNMVLCLM-- 122
 Db 66 VTHDCYKSLKSGCGTKLLKYKSHQGG--QITCS--ANQNSCQKRLCCDCAAAAECEFARN 123
 QY 123 NOTYREYRGFLNVYCGQPTPNC 145
 Db 124 KKTYSLKTYQFYPNMFCKGKPKC 146

RESULT 6

US-09-993-999-8
 ; Sequence 8, Application US/09993999
 ; Patent No. US20020110891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ho, I-Cheng
 ; APPLICANT: Arm, Jonathan P.
 ; APPLICANT: Austen, K. Frank
 ; APPLICANT: Glimcher, Laurie H.
 ; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
 ; TITLE OF INVENTION: Expressed in Th2 Cells
 ; FILE REFERENCE: HUI-046
 ; CURRENT APPLICATION NUMBER: US/09/993,999
 ; PRIOR FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 60/246,316
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 146
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-993-999-8

Query Match 29.6%; Score 283; DB 10; Length 146;
 Best Local Similarity 37.1%; Pred. No. 3.6e-19;
 Matches 53; Conservative 26; Mismatches 56; Indels 8; Gaps 4;

QY 9 ILAGSVLS----TAHGSLLNLKAMVEAVTGRSAILSFVGYCGYGLGGRGQPKDEVDMCC 64
 Db 6 LLAASIMAFGSTQVOGNTAQFGEMIRLTKGRAELSYAFYCGYGLGGRGQPKDEVDMCC 65
 QY 65 HAHDCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKOTCMCDKNMVLCLM-- 122
 Db 66 VTHDCYKSLKSGCGTKLLKYKSHQGG--QITCS--ANQNSCQKRLCCDCAAAAECEFARN 123
 QY 123 NOTYREYRGFLNVYCGQPTPNC 145
 Db 124 KKTYSLKTYQFYPNMFCKGKPKC 146

RESULT 7

US-10-028-072-534
 ; Sequence 534, Application US/10028072
 ; Publication No. US20030004311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.

Mon Feb 10 11:36:15 2003

us-09-975-456b-2.rapb

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063551
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-534

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY 7 VAILAGSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYCYGGLGGRGQPKDEVW 62
Db 3 LALLCGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDATW 62
QY 63 CCHAHDCCYQELFQDQCHPYVDHDTIENNTIIVCSDLNKTCDKQTCMCDKNMVLCLM 122
Db 63 CCQTHDCCYDHLKTQGGCIYKDN-----NKSSIHCHMDLSORYC-----LMAVF 105
QY 123 NOTYRE 128
Db 106 NVIYLE 111

RESULT 9
US-10-123-904-534
Sequence 534, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-534

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

QY 7 VAILAGSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYCYGGLGGRGQPKDEVW 62
Db 3 LALLCGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGGLGGRGQPKDATW 62
QY 63 CCHAHDCCYQELFQDQCHPYVDHDTIENNTIIVCSDLNKTCDKQTCMCDKNMVLCLM 122
Db 63 CCQTHDCCYDHLKTQGGCIYKDN-----NKSSIHCHMDLSORYC-----LMAVF 105
QY 123 NOTYRE 128
Db 106 NVIYLE 111

RESULT 8
US-10-121-049-534
Sequence 534, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

Mon Feb 10 11:36:15 2003

```

; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; FILE OF INVENTION: Expressed in Th2 Cells
; FILE REFERENCE: HUI-046
; CURRENT APPLICATION NUMBER: US/09/993,999
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,316
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-993-999-9

```

```

Query Match 28.5%; Score 272.5; DB 10; Length 137;
Best Local Similarity 37.9%; Pred. No. 3.1e-18;
Matches 53; Conservative 21; Mismatches 61; Indels 5; Gaps 3;

```

```

QY 1 MKKFTVAILAGSVLSTAGHSLNLKAMVEAVTGRSAILSFVGYCYGCGGGRGQPKDEV 60
Db 1 MKGLTLFLWFLACSVPAVPGGLLEKSMIEKVTNRKNAFNYCYCYGCGGGRGTPKDG 60
QY 61 DWCHADCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 120
Db 61 DWCCQMDRCYQGLEEKDCAIRTSYDVRTNGL-VICE--HDSFCPMLCACDRKLYC 117
QY 121 LMNQ--TYREYRGFLNYVC 138
Db 118 LRRNLWTYNPLYQYYPNFC 137

```

RESULT 12

```

US-10-124-591-1
; Sequence 1, Application US/10124591
; Patent No. US20020177208A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; Bandman, Olga
; Guegler, Karl J.
; Shah, Purvi
; Corley, Neil C.

```

```

TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

```

Mon Feb 10 11:36:15 2003

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-534

```

```

Query Match 28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21; Gaps 3;

```

```

QY 7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYCYGCGGGRGQPKDEV 62
Db 3 LALLCGLVVMAGVPIQGGILNLKMKVKQVTGKMPILSYWPGYCHGCGGGRGQPKDATDW 62
QY 63 CCHADCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNMVL 122
Db 63 CQOYHCCYDHLKQCGGIYKDN-----NKSSHCMDSLSQRYC-----LMAYF 105
QY 123 NOTYRE 128
Db 106 NVIYLE 111

```

RESULT 11

```

US-09-993-999-9
; Sequence 9, Application US/09999999
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: Ho, I-Cheng
; APPLICANT: Arm, Jonathan P.

```

```

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-534

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

```


INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVARUT01
CLONE: 816403
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-124-591-1

Query Match 28.1%; Score 268.5; DB 9; Length 165;
Best Local Similarity 34.8%; Pred. No. 8.9e-18;
Matches 47; Conservative 23; Mismatches 62; Indels 3; Gaps 3;
QY 11 AGSVLSTANGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCCHAHDC 70
DB 33 ASRLVHRRGILEAGTVGCGPRTPI-AYMKYCGFCGLGGHQPRAIDWCCHGHDC 91
QY 71 YGELFDQGGHPYVDHYDHTIENNTIEIVCSDLNKTCDKQTCMCKNNVLCMLNQTYREY 130
DB 92 YTRAEAGCSPTERYSNQCVNQS-VLCGPA-ENKQELCKDQETANCLAQTEYNLKY 149
QY 131 RGLNVYCGQPTPNC 145
DB 150 LFYPOFLCEPSPKC 164

RESULT 13
US-09-987-675-5
Sequence 5, Application US/09987675
Patent No. US20020169282A1
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GRFN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,675
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/097,094
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-675-5

Query Match 27.6%; Score 264.5; DB 9; Length 118;
Best Local Similarity 41.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 45; Indels 5; Gaps 3;
QY 22 LLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCCHAHDCYBELFDQGGCHP 81
DB 2 LLDLKSMEIKVTGNALNTNFGYCYGCGWGGRTPKDGTDMCCWAHDHCYGRLEKGCNI 61
QY 82 YVDHYDHTIENNTIEIVCSDLNKTCDKQTCMCKNNVLCMLN--QTYREYRGFLNVYC 138
DB 62 RTQSYKYRFAMGV-VTCEP--GPCHVNLACDRKLVCLKRLNLSYNPOYQYFPNLC 117

RESULT 14
US-09-987-655-5
Sequence 5, Application US/09987655
Patent No. US20020132975A1
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B.H.

APPLICANT: Simon, Reyna
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GRFN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,655
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/097,094
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-655-5

Query Match 27.6%; Score 264.5; DB 10; Length 118;
Best Local Similarity 41.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 45; Indels 5; Gaps 3;
QY 22 LLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDMCCHAHDCYBELFDQGGCHP 81
DB 2 LLDLKSMEIKVTGNALNTNFGYCYGCGWGGRTPKDGTDMCCWAHDHCYGRLEKGCNI 61
QY 82 YVDHYDHTIENNTIEIVCSDLNKTCDKQTCMCKNNVLCMLN--QTYREYRGFLNVYC 138
DB 62 RTQSYKYRFAMGV-VTCEP--GPCHVNLACDRKLVCLKRLNLSYNPOYQYFPNLC 117

RESULT 15
US-09-925-297-511
Sequence 511, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 511
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SITE
LOCATION: (156)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-511

Query Match 23.0%; Score 220.5; DB 10; Length 156;
Best Local Similarity 32.5%; Pred. No. 2.1e-13;
Matches 49; Conservative 23; Mismatches 60; Indels 19; Gaps 7;
QY 3 KFTTVAIL---AGSVLSTANGSLNLKAMVEAV-TGRSAILSFVGYCYGCGLGGRGQPKD 58
DB 10 KLLVLAVLLTVAADSGISPRVWQPRKMKVCPGSDPFLFNNYGYCYGCGLGSGTVPD 69
QY 59 EVDWCCHAHDCYQEQE-----LFDQGGCHPYVDHYDHTIENNTIEIVCSDLNKTCDKQ 109
DB 70 ELDKCCQTHDNCYDQAKLDSCKFLD---NPYTHYTSYSC--SGSAITCSSKNK--ECEAF 124
QY 110 TCMCKNNVLCMLNQTYREYRGFLNVYCQ 139
DB 125 ICNCDRNAACFSPKAPYNKAHNLDTKYYCQ 155

Mon Feb 10 11:36:15 2003

Search completed: February 10, 2003, 10:41:12
Job time : 13 secs

us-09-975-456b-2.rapb

Teater, C.; Warrick, M.W.; Jones, N.D.
submitted to the Brookhaven Protein Data Bank, May 1992
A:Reference number: A51043; PDB:1BBC
A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
R:Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Go
Teater, C.; Warrick, M.W.; Jones, N.D.
Nature 352, 79-82, 1991
A:Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase A2
A:Reference number: A58514; MUID:91287826; PMID:2062381
A:Contents: annotation; X-ray crystallography
C:Genetics:
A:Gene: GDB:PLA2G2A; PLA2B; PLA2L
A:Cross-references: GDB:120296; OMIM:172411
A:Map position: 1p36.1-1p35
A:Introns: 14/1; 62/2; 98/1
C:Function:
A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; extracellular protein; lipid degra
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-144/Product: phospholipase A2 IIA #status experimental <MAT>
F:46-137/48-64,63-117,69-144,70-110,79-103,97-108/Disulfide bonds: #status experiment
F:47,49,51,68/Binding site: calcium (His, Gly, Asp) #status predicted
F:67,111/Active site: His, Asp #status predicted
Query Match 31.6%; Score 302.5; DB 1; Length 144;
Best Local Similarity 38.8%; Pred. No. 7.2e-19;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 3;
QY 1 MKKEFTVAIAGSVLSTAGHSLLNLKAMVEAVTGRSAIISFVGYCYGLGGRGPKDEV 60
DB 1 MKTLLAVIMIFGLQAHGDLNLFHMRKLTGKRAALSYGFYCHGCGVGRGPKDAT 60
QY 61 DWCHAHDCYQELFDQGCCHPYVDHYDHTIENNTIEVCSDLNKTCDKOTCMDCNMVLC 120
DB 61 DRCCVTHDCYKLEKRGCGTKFLSYKFS-NSGRITCA--KQDSRSLCECDKAAATC 117
QY 121 LMNQ--TYREYRGLNVCYCGPTPNC 145
DB 118 FARNKTTYNKQYYSNKHCRGSTPRC 144
RESULT 3
PSTVXF
phospholipase A2 (EC 3.1.1.4) X - habu
N:Alternate names: phosphatidylcholine 2-acylhydrolase
C:Species: Trimeresurus flavoviridis (habu)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Apr-1998
C:Accession: A25500
R:Kini, R.M.; Kawabata, S.I.; Iwanaga, S.
Toxicon 24, 1117-1129, 1986
A:Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
A:Reference number: A94320; MUID:87179112; PMID:3564060
A:Accession: A25500
A:Molecule type: protein
A:Residues: 1-122 <KIN>
C:Function:
A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metall
F:26-122,28-44,43-95,49-115,50-88,57-81,75-86/Disulfide bonds: #status predicted
F:27,29,31,48/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F:47,89/Active site: His, Asp #status predicted
Query Match 31.2%; Score 298.5; DB 1; Length 122;
Best Local Similarity 41.3%; Pred. No. 1.4e-18;
Matches 52; Conservative 23; Mismatches 44; Indels 7; Gaps 4;
QY 22 LLNLKAMVEAVTGRSAIISFVGYCYGLGGRGPKDEVDMCCHAHDCYQELFDQGCCHP 81
DB 22 LLNLKAMVEAVTGRSAIISFVGYCYGLGGRGPKDEVDMCCHAHDCYQELFDQGCCHP 81

A:Residues: 1-144 <KRA>
A:Accession: B32862
A:Molecule type: protein
A:Residues: 21-39 <KRA>
A:Note: this protein was also detected in platelets
R:Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.
Adv. Exp. Med. Biol. 275, 35-53, 1990
A:Title: Structure and properties of a secreted platelet phospholipase A-2 from human platelets
A:Reference number: A60266; MUID:91050834; PMID:2239446
A:Accession: A60266
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-144 <KR3>
R:Seilhamer, J.J.; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
J. Biol. Chem. 264, 5335-5336, 1989
A:Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
A:Reference number: A32847; MUID:89174566; PMID:2925608
A:Accession: A32847
A:Molecule type: mRNA
A:Residues: 1-144 <SEI>
A:Cross-references: GB:J04704; EMBL:M22430; NID:g190888; PIDN:AAA36550.1; PID:g190889
R:Crowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R.
Adv. Exp. Med. Biol. 279, 173-184, 1990
A:Title: Isolation and characterization of cDNA clones from human placenta coding for ph
A:Reference number: A60263; MUID:91263879; PMID:1710670
A:Accession: A60263
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-144 <CRO>
R:Lai, C.Y.; Wada, K.
Biochem. Biophys. Res. Commun. 157, 488-493, 1988
A:Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
A:Reference number: A31350; MUID:89076274; PMID:3202859
A:Accession: A31350
A:Molecule type: protein
A:Residues: 21-33 <LAI>
R:Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
J. Biochem. 104, 326-328, 1988
A:Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip
A:Reference number: PT0056; MUID:89197814; PMID:3240982
A:Accession: PT0056
A:Molecule type: protein
A:Residues: 21-46, 'X', 48-54 <HAR>
R:Kanda, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
Biochem. Biophys. Res. Commun. 163, 42-48, 1989
A:Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
A:Reference number: A32913; MUID:89374261; PMID:2775276
A:Accession: A32913
A:Molecule type: protein
A:Residues: 21-144 <KAN>
R:Parks, T.P.; Lukas, S.; Hoffman, A.F.
Adv. Exp. Med. Biol. 275, 55-81, 1990
A:Title: Purification and characterization of a phospholipase A-2 from human osteoarthr
A:Reference number: A60265; MUID:91050835; PMID:2146857
A:Accession: A60265
A:Molecule type: protein
A:Residues: 21-45, 'X', <PAR>
R:Recklies, A.D.; White, C.
Arthritis Rheum. 34, 1106-1115, 1991
A:Title: Phospholipase A-2 is a major component of the salt-extractable pool of matrix H
A:Reference number: A61201; MUID:92029121; PMID:1930329
A:Accession: A61201
A:Molecule type: protein
A:Residues: 21-40 <REC>
R:Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.F.
Inflammation 15, 355-366, 1991
A:Title: Circulating phospholipase A-2 activity associated with sepsis and septic shock
A:Reference number: A61634; MUID:92098137; PMID:1757123
A:Accession: A61634
A:Molecule type: protein
A:Residues: 21-44 <GRE>
R:Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods

Db 2 LLOFRKMKWTKGKPIVAFVGCYCGKGRGPKDTRCCFVHDDCCYEKV--TGCDP 59
 QY 82 YVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNMVLCLMN--QTYREERYGFLNVYQC 139
 Db 60 KWSYYSYISLNG--DIVCG--GDPYCTKVKCECDKAAICFRDNLKTYKNRYMTEPDIFCT 116
 QY 140 GTPPNC 145
 Db 117 DPTEGC 122

RESULT 4

I48093
 phospholipase A2 (EC 3.1.1.4) type II - guinea pig
 C:Species: Cavita porcellus (guinea pig)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999
 C:Accession: I48093
 R:Vial, D.; Senorato-Pose, M.; Havet, N.; Molio, L.; Vargaftig, B.B.; Touqui, L.
 J. Biol. Chem. 270, 17327-17332, 1995
 A:Title: Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regulation by interferon-gamma
 A:Reference number: I48093; MUID:95340522; PMID:7615534
 A:Accession: I48093
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-145 <RES>
 A:Cross-references: EMBL:X82631; NID:9951010; PIDN:CAA57953.1; PID:9951011
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase
 F:67.112/Active site: His, Asp #status predicted

Query Match 31.0%; Score 297; DB 2; Length 145;
 Best Local Similarity 37.4%; Pred. No. 2.1e-18;
 Matches 55; Conservative 23; Mismatches 65; Indels 4; Gaps 3;
 QY 1 MKKFTVATAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGGLGGRGQPKDEV 60
 Db 1 MKLLLLLVNASDLPQAHGHLKQFTTEMIKLTGKNGLTSGYAGYCHGCGVGGRTPKDAT 60
 QY 61 DWCHADCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNMVLCL 120
 Db 61 DRCCVRHDCYDRLMKRGCGTKFLNYRFT-HKGSITCS-VKQNSCQKQLCEDKAAAYC 118
 QY 121 LMN--QTYREERYGFLNVYCGPTPNC 145
 Db 119 FAANLKSYSRRYQFYNGLCRGKTPSC 145

RESULT 5

A35493
 phospholipase A2 (EC 3.1.1.4) II precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 14-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 18-Jun-1999
 C:Accession: A35493; S11388; S71310
 R:Komada, M.; Kudo, I.; Inoue, K.
 Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990
 A:Title: Structure of gene coding for rat group II phospholipase A-2.
 A:Reference number: A35493; MUID:90267443; PMID:2346480
 A:Accession: A35493
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <KOM>

A:Cross-references: GB:M37127; NID:9204318; PIDN:AAA41223.1; PID:g204319
 A:Note: the authors translated the codon TAT for residue 42 as Thr
 R:Kusunoki, C.; Sato, S.; Kobayashi, M.; Niwa, M.
 Biochim. Biophys. Acta 1087, 95-97, 1990
 A:Title: Structure of genomic DNA for rat platelet phospholipase A(2).
 A:Reference number: S11388; MUID:90381322; PMID:2400792
 A:Accession: S11388
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <KUS>
 A:Cross-references: EMBL:X51529; NID:956930; PIDN:CAA35909.1; PID:g56931
 R:Aarsman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch

Arch. Biochem. Biophys. 331, 95-103, 1996
 A:Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from rat platelet
 A:Reference number: S71310; MUID:96268465; PMID:8660688
 A:Accession: S71310
 A:Molecule type: protein
 A:Residues: 22-29, 'X', '31-32, 'X', '34 <AAR>
 A:Experimental source: kidney
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase; lipid degradation
 F:68.113/Active site: His, Asp #status predicted

Query Match 30.8%; Score 294.5; DB 2; Length 146;
 Best Local Similarity 42.3%; Pred. No. 3.5e-18;
 Matches 60; Conservative 20; Mismatches 55; Indels 7; Gaps 5;
 QY 7 VAILA-GSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGGLGGRGQPKDEVWCCH 65
 Db 9 VVIMAFGSI--QVQGSLLLEFGQMLFKTKRADVSYGFYCHGCGVGGSPKDATDWCCV 66
 QY 66 AHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNMVLCLM--N 123
 Db 67 THDCCYNRLKRGCGTKFLTYKFSYRGG-QISCS-TNQDSCRKQLCCQDKAAAECAFARK 124
 QY 124 QTYREERYGFLNVYCGPTPNC 145
 Db 125 KSYSLKYQFYLNKFKCKGKTPSC 146

RESULT 6

A33394
 phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
 C:Accession: A33394; JU0131
 R:Ishizaki, J.; Ohara, O.; Nakamura, E.; Tamaki, M.; Ono, T.; Kanda, A.; Yoshida, N.; Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989
 A:Title: cDNA cloning and sequence determination of rat membrane-associated phospholipase A2
 A:Reference number: A33394; MUID:89350908; PMID:2764915
 A:Accession: A33394
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-146 <ISH>
 A:Cross-references: GB:M25148
 R:Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
 J. Biochem. 106, 545-547, 1989
 A:Title: Structure of cDNA coding for rat platelet phospholipase A2.
 A:Reference number: JU0131; MUID:90110043; PMID:2606907
 A:Accession: JU0131
 A:Molecule type: mRNA
 A:Residues: 1-146 <KOM>
 A:Cross-references: GB:D00523; NID:g220857; PIDN:BAA00410.1; PID:g220858
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-146/Product: phospholipase A2 #status predicted <MAT>
 F:68.113/Active site: His, Asp #status predicted

Query Match 30.0%; Score 287.5; DB 2; Length 146;
 Best Local Similarity 41.5%; Pred. No. 1.4e-17;
 Matches 59; Conservative 20; Mismatches 56; Indels 7; Gaps 5;
 QY 7 VAILA-GSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGGLGGRGQPKDEVWCCH 65
 Db 9 VVIMAFGSI--QVQGSLLLEFGQMLFKTKRADVSYGFYCHGCGVGGSPKDATDWCCV 66
 QY 66 AHDCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNTECDKQTCMCDKNMVLCLM--N 123
 Db 67 THDCCYNRLKRGCGTKFLTYKFSYRGG-QISCS-TNQDSCRKQLCCQDKAAAECAFARK 124
 QY 124 QTYREERYGFLNVYCGPTPNC 145
 Db 125 KSYSLKYQFYLNKFKCKGKTPSC 146

A;Molecule type: mRNA
A;Residues: 1-138 <TSA>
A;Cross-references: EMBL:X77645
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;6.3.1.95/Active site: His. Asp #status predicted

Query Match	29.3%	Score 280.5;	DB 2;	Length 138;
Best Local Similarity	37.4%	Pred. No. 5.2e-17;		
Matches 55; Conservative	29;	Mismatches 52;	Indels 11;	Gaps 5;

[illegible]

RESULT 9

S68429
myotoxin precursor - southern copperhead
C:Species: Agkistrodon contortrix contortrix (southern copperhead)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: S68429 S74296
R:de Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A:Title: cDNA cloning and sequence analysis of a lysine-49 phospholipase A(2) myotoxin
A:Reference number: S68429. PMID:96154243; PMID:8579368

A;Accession: S00425
A;Molecule type: mRNA
A;Residues: 1-137 <DEA>
A;Cross-references: EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g809485
A;Accession: S74296

A:Residues: 17-36 <DER>
C:Superfamily: phospholipase A2
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-127/Domain: myotoxin #status experimental <MAT>

Query Match	29.2%;	Score 279.5;	DB 2;	Length 137;
Best Local Similarity	39.9%;	Pred. No. 6.3e-17;		
Matches 57;	Conservative	23;	Mismatches 52;	Indels 11;
				Gaps 5;

QY

1 MKKFTTVAIIAGSVLSTAHGSLNLNKAMVEAVTGRSAILSFVGYGCVCGGLGGRGPKDEV 60
| : | :: ||||| | : |::| : |::| : |::| : |::| : |::| : |::| : |::| : |::| :
SF

1 MDTMTVTATVIV---LVGVVGESLIIEIGKMILIOETGNNAITSYGSGCNCGWHRGPCKDAT 56

[illegible]

57 DRCCFVHKCCYKLTLD--CNHKTDRYSYSWKNA-IICEE--KNPCLKMECCDRAVAIC 111

QY 121 LMN--QTYREERYGFLNYYCGP 141

Db 132 L : : : : : 134

PRECISE 10

PSABA
 phospholipase A2 (EC 3.1.1.4) - mamushi
 N:Alternate names: phosphatidylcholine 2-acylhydrolase
 C:Species: Agkistrodon blomhoffii (mamushi)
 C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 26-Feb-1999
 C:Accession: A00766; S43474
 R:Forst, S.; Weiss, J.; Blackburn, P.; Frangione, B.; Goni, F.; Elsbach, P.
 Biochemistry 25, 4309-4314, 1986
 A:Title: Amino acid sequence of a basic Agkistrodon haysi blomhoffii phospholipase A2
 A:Reference number: A00766; MUID:87000546; PMID:3530322

RESULT 7
I48342
Phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48342 #sequence S35948: I49352
R:Wulferink, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A:Title: Enhancing factor of a Paneth cell specific protein from mouse small intestines: F

A:Accession: I48342
A>Status: Preliminary; translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 1-146 <MOL1>
A:Cross-references: EMBL:X74266; NID:g557247; PIDN:CAA52325.1; PID:g557248
K:Mulharkat, R.; Res Commun 197, 351-352, 1993.
Biochem. Enhancing factor, a peneth cell specific protein
N:Reference number: PMID:94071967; PMID:84350944

A;Accession: PC2009
A;Molecule type: mRNA
A;Residues: 22-146 <MUL2>
A;Note: correction of S35948
R;Mulharkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo, M.
submitted to the EMBL Data Library, July 1993
A;Reference number: S35948

A: Accession: S35948
A: Molecule type: mRNA
A: Residues: 25-115, 'R', 118-146 <MUL3>
A: Cross-references: EMBL: X74266
B: Kennedy, B. P.; Payette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C. C.
J. Biol. Chem. 270, 22378-22385, 1995
A: Title: A natural disruption of the secretory A2 gene in inbred
B: Reference number: 149452; MUID: 95403435; PMID: 7673223

A:Accession: I49332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18, 'V', 20-85, 'K', 87-146 <KEN>
A:Cross-references: EMBL:U32358; NID:984836; PTDN:AAC52252.1; PID:984837
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:68.113/Active site: His, Asp #status predicted

Query Match 29.4%; Score 281; DB 2; Length 146;
Best Local Similarity 37.1%; Pred. No. 5e-17;
Matches 53; Conservative 26; Mismatches 56; Indels 8; Gaps 4;

QY

9 ILAGSVLSTA-----HGSLNLNKARVEAVTGRSAILSFVGYCYCGLGGRQPKEVDWCC 64
 :
 :
 :

DH

6 IIAASTMAFGSITODOGNTAAOFGEMIRLTGTCKRAEISYAIFYCHCGCLGGKGSFKDATRCCC 65
 :
 :
 :

[illegible]

66 VTHDCYSLSEKSGCGTALLETIRKISHUGG QILCS ANQSCQKNCQCCGCGGATGCGTATTTT TTTT

Db

QY 123 NOTYREERYGFLNVYCOGPTPNC 145

124 KKTYSLKYOFPNMFCKGKKPKC 146

Db

RESULT 8

S59522
phospholipase A2 (EC 3.1.1.4) precursor - Chinese habu
C.Species: Trimeresurus mucrosquamatus (Chinese habu)
C.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 07-May-1999
C.Accession: S59522
R.Tsai, L.H.; Lu, R.J.; Wang, Y.M.; Ho, C.L.; Liaw, L.L.
Biochem. J. 311, 895-900, 1995
A.Title: Molecular cloning and characterization of a neurotoxic phospholipase A(2) from
A.Reference number: S59522; MUID:96067607; PMID:7487947
A.Accession: S59522
A>Status: preliminary

Query Match	28.8%	Score	275.5	DB 2	Length	138
Best Local Similarity	37.9%	Pred. No.	1.4e-16			
Matches	53	Conservative	22	Mismatches	60	Indels
QY	1	MKKFFTVAILAGSVLSTAHGSLNLNKA	VEAVTGRSAILSFVGYCGYGLGGRGQPKDEV	60		
Db	1	MKGLLPFLAWFLACSVPAVOGGLDLK	SMIEKVTKNALTNYGFYCGYGGRGRTPKDGT	60		
QY	61	DMCCHAHDCCYQELPDGCHPVVDHYDHT	INNNTEIIVCSDLNKTECDKQTCMCDKNWJLC	121		
Db	61	DMCCWAHDHCYGRLEEKGCNTRTSQYKRFAMGV	-VTCEP--GPFCHVNLCAADRKLVC	11		
QY	121	LMN--QTYREYRGFLNVC	138			
			:	:	:	:
			:	:	:	:

PRRST
 phospholipase A2 homolog crotoxin acidic subunit precursor - tropical rattlesnake
 C:Species: Crotalus durissus terrificus (Tropical rattlesnake, cascabel)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
 C:Accession: S01392; A23861; S11382; B23861; C23861
 R:Bouchier, C.; Ducancel, F.; Guignery-Frelat, G.; Bon, C.; Boulain, J.C.; Menez, A.
 Nucleic Acids Res. 16, 9050, 1988
 A:Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin.
 A:Reference number: S01392; MUID:89016587; PMID:3174444
 A:Accession: S01392
 A:Molecule type: mRNA
 A:Residues: 1-138 <BOU>
 A:Cross-references: EMBL:X12606; NID:g62685; PIDN:CAA31126.1; PID:g62686
 R:Aird, S.D.; Kaiser, I.I.; Lewis, R.V.; Kruggel, W.G.
 Biochemistry 24, 7054-7058, 1985
 A:Title: Rattlesnake presynaptic neurotoxins: primary structure and evolutionary origin
 A:Reference number: A30500; MUID:86104201; PMID:4084559
 A:Accession: A23861
 A:Molecule type: protein
 A:Residues: 39-73, 'N', 75-76, 'XXXXXXX', 95-102, 'G', 104-118, 125-138 <AIR>
 R:Aird, S.D.; Yates III, J.R.; Martino, P.A.; Shabowitz, J.; Hunt, D.F.; Kaiser, I.I.
 Biochim. Biophys. Acta 1040, 217-224, 1990
 A:Title: The amino acid sequence of the acidic subunit B-chain of crotoxin.
 A:Reference number: S11382; MUID:90381276; PMID:2400773
 A:Accession: S11382
 A:Molecule type: protein
 A:Residues: 1-7, 85-118 <AIR2>
 C:Comment: This subunit has no enzymatic or toxin activity. It helps target crotoxin base
 C:Complex: heterodimer of acidic and basic subunits; mature acidic subunit has 3 chains,
 C:Superfamily: phospholipase A2
 C:Keywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom
 C:Keywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-38/Domain: propeptide #status predicted <PRO>
 F:39-76, 84-118, 125-138/Product: crotoxin acidic subunit #status experimental <MAT>
 F:39-76/Domain: crotoxin acidic subunit chain A #status experimental <CHA>

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:27 ; Search time 12 Seconds
(without alignments)
580.669 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCSHQSPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	957	100.0	168	1 PA2F_HUMAN	Q9bzm2 homo sapien
2	747	78.1	168	1 PA2F_MOUSE	Q9qzt4 mus musculu
3	353	36.9	145	1 PA2D_HUMAN	Q9unk4 homo sapien
4	344.5	36.0	144	1 PA2D_MOUSE	Q9wvf6 mus musculu
5	319.5	33.4	138	1 PA2X_TRIFL	Q02517 trimeresuru
6	313.5	32.8	142	1 PA2E_MOUSE	Q9qul3 mus musculu
7	309	32.3	142	1 PA2E_HUMAN	Q9nzk7 homo sapien
8	302.5	31.6	144	1 PA2A_HUMAN	P06860 trimeresuru
9	298.5	31.2	122	1 PA2X_TRIFL	P47711 cavia porce
10	297	31.0	145	1 PA2M_CAVPO	Q9qxx3 mus musculu
11	287.5	30.0	146	1 PA2A_RAT	P14423 rattus norv
12	283.5	29.6	151	1 PA2X_MOUSE	Q48076 mus musculu
13	282	29.5	150	1 PA2X_MOUSE	Q9qzt3 rattus norv
14	282	29.5	151	1 PA2X_RAT	P37391 mus musculu
15	281	29.4	146	1 PA2A_MOUSE	P49121 agkistrodon
16	280.5	29.3	137	1 PA25_MOUSE	P04417 agkistrodon
17	279.5	29.2	137	1 PA2M_AKCL	P45881 bothrops ja
18	278.5	29.1	122	1 PA2L_AKHA	P39877 homo sapien
19	278.5	29.1	138	1 PA2L_BOTJR	P08878 crotalus du
20	275.5	28.8	138	1 PA25_HUMAN	P11407 vipera ammo
21	272.5	28.5	138	1 PA2A_CRODU	Q9pve3 bothrops as
22	272.5	28.5	138	1 PA2C_VIPAA	P70088 trimeresuru
23	272	28.4	138	1 PA23_BOTAS	P48650 echis carin
24	272	28.4	138	1 PA26_TRIGA	P51433 rattus norv
25	269.5	28.2	122	1 PA2N_ECHA	P00626 vipera ammo
26	268.5	28.1	137	1 PA25_RAT	O15496 homo sapien
27	268.5	28.1	138	1 PA2A_VIPAA	P17935 vipera ammo
28	268.5	28.1	155	1 PA2X_HUMAN	P39878 rattus norv
29	267.5	28.0	138	1 PA2L_VIPAA	P04361 agkistrodon
30	267	27.9	150	1 PA2C_RAT	Q91834 bothrops mo
31	264.5	27.6	121	1 PA2H_AKPI	P51972 agkistrodon
32	262	27.4	122	1 PA22_BOTMO	
33	261.5	27.3	123	1 PA21_AKPI	

34	261.5	27.3	138	1 PA2B_VIPAA	P14424 vipera ammo
35	260	27.2	122	1 PA22_AKHA	P20249 agkistrodon
36	259.5	27.1	122	1 PA21_BOTAS	P20474 bothrops as
37	258	27.0	138	1 PA2B_TRIFL	P20381 trimeresuru
38	257.5	26.9	121	1 PA22_BOTAS	P24605 bothrops as
39	256.5	26.8	121	1 PA22_BOTPI	P82287 bothrops pi
40	255.5	26.7	138	1 PA21_TRIGA	P20476 trimeresuru
41	252.5	26.4	121	1 PA21_BOTPI	P58399 bothrops pi
42	251.5	26.3	138	1 PA2B_CRODU	P07517 crotalus du
43	250.5	26.2	121	1 PA2H_BOTJR	Q90249 bothrops ja
44	250.5	26.2	122	1 PA2_VIPBB	P31854 vipera beru
45	249.5	26.1	138	1 PA2A_VIPAA	Q98996 vipera pala

ALIGNMENTS

RESULT 1

PA2F_HUMAN					
ID	PA2F_HUMAN	STANDARD;	PRT;	168	AA.
AC	Q9BZM2; Q9H506;				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Group IIF secretory phospholipase A2 precursor (EC 3.1.1.4)				
DE	(Phosphatidylcholine 2-acylhydrolase GIIF) (GIIF SPLA2) (SPLA(2)-IIF).				
GN	PLA2G2F.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.				
RX	MEDLINE=20563827; PubMed=11112443;				
RA	Valentin E., Singer A.G., Ghomashchi F., Lazdunski M., Gelb M.H.,				
RA	Lambeau G.;				
RT	"Cloning and recombinant expression of human group IIF-secreted				
RT	phospholipase A(2).";				
RL	Biochem. Biophys. Res. Commun. 279:223-228(2000).				
RN	[2]				
RP	SEQUENCE OF 1-98 FROM N.A.				
RA	Wallis J.;				
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.				
CC	-I- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-				
CC	acyl groups in 3-sn-phosphoglycerides. Hydrolyzes				
CC	phosphatidylglycerol versus phosphatidylcholine with a 15-fold				
CC	preference.				
CC	-I- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-				
CC	acylglycerophosphocholine + a fatty acid anion.				
CC	-I- COFACTOR: Binds 1 calcium ion per subunit.				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- TISSUE SPECIFICITY: Expressed at high levels in placenta, testis,				
CC	thymus and at lower levels in heart, kidney, liver and prostate.				
CC	-I- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF306556; AAC50242.1;				
DR	EMBL; AL158172; CAC13160.1; ALT_INIT.				
DR	HSPF; P82287; IQLL.				
DR	InterPro; IPR001211; PhospholipaseA2.				
DR	Pfam; PF00068; phoslip; 1.				
DR	PRINTS; PR00389; PHPLIPASEA2				
DR	ProDom; PD000303; PhospholipaseA2				
DR	SMART; SMO0085; PA2c; 1.				
DR	PROSITE; PS00119; PA2_ASP; FALSE_NEG.				
DR	PROSITE; PS00118; PA2_HIS; 1.				

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 CC EMBL; AF166099; AAF04500.2; -
 CC HSSP; P00593; 4BP2.
 CC MG; MG1.1349661; pla2q2f.
 CC InterPro: IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; phoslip; 1
 CC PRINTS; PR00389; PHPHLIPASEA2.
 CC PRODOM; PD000303; PhospholipaseA2; 1.
 CC SMART; SM00085; PA2c; 1.
 CC PROSITE; PS00119; PA2_ASP; FALSE_NEG.
 CC PROSITE; PS00118; PA2_HIS; 1.
 CC Hydrolase; Lipid degradation; Signal; Calcium.
 KW SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 168 GROUP IIF SECRETORY PHOSPHOLIPASE A2.
 FT ACT_SITE 67 67 BY SIMILARITY.
 FT ACT_SITE 114 114 BY SIMILARITY.
 FT DISULFID 46 138 BY SIMILARITY.
 FT DISULFID 48 64 BY SIMILARITY.
 FT DISULFID 63 120 BY SIMILARITY.
 FT DISULFID 69 145 BY SIMILARITY.
 FT DISULFID 70 113 BY SIMILARITY.
 FT DISULFID 79 106 BY SIMILARITY.
 FT DISULFID 98 111 BY SIMILARITY.
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 51 51 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 68 68 BY SIMILARITY.
 SQ SEQUENCE 168 AA; 18880 MW; 9E15FB6AC0F5450C CRC64;
 Query Match 78.1%; Score 747; DB 1; Length 168;
 Best Local Similarity 75.2%; Pred No. 2,8e-60;
 Matches 124; Conservative 20; Mismatches 21; Indels 0; Gaps 0

QY 1 MKKFTTVAIIAGSVLSTAHSGSLNLKAMAEVTVGRSAILSFVGYGCGYGLGGRGOPKDEV 60
 Db 1 MKKFEATVLAGSVVTTAHSLLNLKSMVEATHRNSILSFVGYGCGYGLGGRGHPMDEV 60

QY 61 DWCHAHDCYQELFDGCGHPYVDHDTTENTNTEVSDLNKTECDKQTCMCKNNVLC 120
 Db 61 DWCHAHDCYQELFDGCGHPYVDHDTTENTNTEVSDLNKTECDKQTCMCKNNVLC 120

QY 121 LMNQTREYRGFLNVYCGQPTNCISYEPPEVTCVSHOSPAPP 165
 Db 121 LKDHPIENKRYGVNVCYCGPTNCISYDYPPEVTCVGHGLPATP 165

RESULT 3
 ID PA2D_HUMAN STANDARD; PRT; 145 AA.
 AC Q9UNK4; Q9UK01;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Group IID secretory phospholipase A2 precursor (BC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
 DE (sPLA2)-IID) (Secretory-type PLA, stroma-associated homology).
 DE PLA2GD2 OR SPLASH.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Carnivora; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.; VARIANT GLY-80, AND CHARACTERIZATION.
 RX MEDLINE=93386983; PubMed=10455175;
 RA Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,


```

Best Local Similarity 45.18; Pred. No. 3e-24;
Matches 65; Conservative 52; Indels 7; Gaps 4;

QY 7 VAILAGSVL---STAHGSLNLKAMVEAVTGRSAILSFGVGYCGLGGGQPKDEVDWC 63
Db 3 LALLGCLLAGITATOGGLNLNKNVTHMTGKKAFFSYWPGYCGHGLGGGQPKDATDWC 62
QY 64 CHAHDCCYQELFDQGGHPYVHYDHTFIENNTFIVCSDLNKTECDKOTCMCDKNVVLCLMN 123
Db 63 CQKHDCCYAHLKIDGKSLTDNYKYSISQGT-IQCS-D-NGSWCEKQLCACDKEVALCLQK 120
QY 124 --QTYEEYRGFLNVYCGQPTPNC 145
Db 121 NLDYSYNKRLRYWYRPRCKGKTFAC 144

RESULT 5
PA2Y_TRIFL
ID PA2Y_TRIFL STANDARD; PRT; 138 AA.
AC AC Q02517;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2 isozyme PL-X' precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimeresurus.
NCBI_TaxID=88087;
[1]
SEQUENCE FROM N.A.
EP MEDLINE=92409555; PubMed=1528861;
RA Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sakaki Y.,
RA "Kihara H., Ono M.;
RA "Unusually high conservation of untranslabeled sequences in cDNAs for
RA Trimeresurus flavoviridis phospholipase A2 isozymes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561(1992).
CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D10721; BAA01564.1; -.
CC HSSP; P51972; IVAP.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR Hydrolase; Lipid degradation; Calcium; Multigene family; Venom;
KW SIGNAL.
FT 1 16 PHOSPHOLIPASE A2 ISOZYME PL-X'.
FT CHAIN 17 138 BY SIMILARITY.
FT ACT_SITE 63 63 BY SIMILARITY.
FT ACT_SITE 105 105 BY SIMILARITY.
FT DISULFID 42 131 BY SIMILARITY.
FT DISULFID 44 60 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 65 138 BY SIMILARITY.

```

FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT CA_BIND 43 43 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 45 45 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 64 64 BY SIMILARITY.
 SQ SEQUENCE 138 AA; 15733 MW; 471B01878CCA1EDI CRC64;

 Query Match 33.4%; Score 319.5; DB 1; Length 138;
 Best Local Similarity 40.1%; Pred. No. 5e-22;
 Matches 59; Conservative 28; Mismatches 49; Indels 11; Gaps 5;

 QY 1 MKKFTVAILAGSVLSTAGHSLNLANKAVEAVTGRSAILSVGVGCGGLGGRGQPKDEV 60
 Db 1 MRTLIMAVL-----LVGVEGHLQFRKMKKMTGKEPIVSFAFYGCYCGGGRGPKDAT 56

 QY 61 DWCHAHDCCYQELFDQCHPYVDHYDHTIENNTVCSDLNKTECDKQTCMDCKNMVLC 120
 Db 57 DRCCFVHDCCEKV--TCGDKRWDTYTSSENG-DIVCGGDN--PCTKEVCECDKAAIC 111

 QY 121 LMN--QTYREYRGFLNVYCGPTPNC 145
 Db 112 FRDLNLTYYKKRYMTFDFCTDPTTEK 138

 RESULT 6
 PAZE_MOUSE STANDARD; PRT; 142 AA.
 AC Q90L3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIIE) (SPLA(2)-IIE).
 GN PLA2G2E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=2002639; PubMed=10531313;
 RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
 RT "On the diversity of secreted phospholipases A2. Cloning, tissue
 RT distribution, and functional expression of two novel mouse group II
 RT enzymes.";
 RL J. Biol. Chem. 274:31195-31202(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=HALB/C;
 RX MEDLINE=20148788; PubMed=10681567;
 RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
 RA Fujii N., Kawamoto K., Hanasaki K.;
 RT "Structures, enzymatic properties, and expression of novel human and
 RT mouse secretory phospholipase A(2)s.";
 RL J. Biol. Chem. 275:5785-5793(2000).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower
 CC levels in various other tissues.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF166098; AAF04499.1; -;
 DR EMBL: AF112984; AAF22290.1; -;
 DR HSSP: P14555; IPOD.
 DR MGD: MGI:1349660; Pla2g2e.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF00068; phoslip.1
 DR PRINTS: PR00389; PHPLIPASEA2.
 DR ProDom: PD000303; PhospholipaseA2; 1.
 DR SMART: SM00085; PA2c; 1.
 DR PROSITE: PS00119; PA2_ASP; FALSE_NEG.
 DR PROSITE: PS00118; PA2_HIS; 1.
 KW Hydrolase; Lipid degradation; Signal; Calcium.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.
 FT ACT_SITE 65 65 BY SIMILARITY.
 FT ACT_SITE 109 109 BY SIMILARITY.
 FT DISULFID 44 135 BY SIMILARITY.
 FT DISULFID 46 62 BY SIMILARITY.
 FT DISULFID 61 115 BY SIMILARITY.
 FT DISULFID 67 142 BY SIMILARITY.
 FT DISULFID 68 108 BY SIMILARITY.
 FT DISULFID 77 101 BY SIMILARITY.
 FT DISULFID 95 106 BY SIMILARITY.
 FT CA_BIND 45 45 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 66 66 BY SIMILARITY.
 SQ SEQUENCE 142 AA; 15942 MW; 8B0E3CC710A1F946 CRC64;

 Query Match 32.8%; Score 313.5; DB 1; Length 142;
 Best Local Similarity 42.2%; Pred. No. 1.8e-21;
 Matches 62; Conservative 20; Mismatches 58; Indels 7; Gaps 5;

 QY 1 MKKFTVAILAGSVLSTAGHSLNLANKAVEAVTGRSAILSVGVGCGGLGGRGQPKDEV 60
 Db 1 MKFPALACLC-LVPLAGLNLGVFGVMIERMTGKPA-LQYNDYGCYCGVGGSHWPVDET 58

 QY 61 DWCHAHDCCYQELFDQCHPYVDHYDHTIENNTVCSDLNKTECDKQTCMDCKNMVLC 120
 Db 59 DWCHAHDCCYGRLEKLGCDPKLEKYLFSITRD-NIFCA--GRTACQRTCECDKRAALC 115

 QY 121 LMN--QTYREYRGFLNVYCGPTPNC 145
 Db 116 FRNLNTYRKAYAHYPNKLCCTGTPTTC 142

 RESULT 7
 PAZE_HUMAN STANDARD; PRT; 142 AA.
 AC Q9NZK7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIIE) (SPLA(2)-IIE).
 GN PLA2G2E.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=20148788; PubMed=10681567;
 RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
 RA Fujii N., Kawamoto K., Hanasaki K.;
 RT "Structures, enzymatic properties, and expression of novel human and
 RT mouse secretory phospholipase A(2)s.";
 RL J. Biol. Chem. 275:5785-5793(2000).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Has a preference for
 CC arachidonic-containing phospholipids.

Mon Feb 10 11:36:18 2003

```

CC -|- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -|- COFACTOR: Binds 1 calcium ion per subunit.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and
CC placenta.
CC -|- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF19279; AAF36541.1; -.
CC HSP; P14555; IPOD.
CC InterPro; IP001211; PhospholipaseA2.
CC Pfam; PF00068; phoslip; 1.
CC PRINTS; PR00389; PHPLIPASEA2.
CC PRODOM; PD000303; PhospholipaseA2; 1.
CC SMART; SM00085; PA2c; 1.
CC PROSITE; PS00119; PA2_ASP; FALSE_NEG.
CC PROSITE; PS00118; PA2_HIS; 1.
CC Hydrolase; Lipid degradation; Signal; Calcium.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.
CC FT ACT_SITE 65 65 BY SIMILARITY.
CC FT ACT_SITE 109 109 BY SIMILARITY.
CC FT DISULFID 44 135 BY SIMILARITY.
CC FT DISULFID 46 62 BY SIMILARITY.
CC FT DISULFID 61 115 BY SIMILARITY.
CC FT DISULFID 67 142 BY SIMILARITY.
CC FT DISULFID 68 108 BY SIMILARITY.
CC FT DISULFID 77 101 BY SIMILARITY.
CC FT DISULFID 95 106 BY SIMILARITY.
CC FT CA_BIND 45 45 VIA CARBONYL OXYGEN (BY SIMILARITY).
CC FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).
CC FT CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).
CC FT CA_BIND 66 66 BY SIMILARITY.
CC SEQUENCE 142 AA; 15989 MW; 3C360EA710E141FB CRC64;
CC -----
Query Match 32.3%; Score 309; DB 1; Length 142;
Best Local Similarity 43.8%; Pred. No. 4.5e-21;
Matches 56; Conservative 18; Mismatches 48; Indels 6; Gaps 4;
CC QY 20 GSLLNLKAMVEAVTGRSAILSPVGYGCGYGLGGQPKDEVDCCHAHDCYQELFDGCG 79
CC |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
CC Db 19 GNLVQGVMIERKWTCKSA-LOVNDYGCYGGSHWPVDQTDWCCCHAHDCYGRLEKLCG 77
CC QY 80 HPVVDHYDHTIENNTIVCSDLNTECDKQTCMCDKNVCLMNO--TYREYRGFLNVY 137
CC |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
CC Db 78 EPKLEKLYFSV-SERGIFCA--GRITTCQRLTCECDKRAALCFRRNLGTYNKRKYAHYFNKL 134
CC QY 138 CQGPTEPC 145
CC |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
CC Db 135 CTGPTTTC 142
CC -----
RESULT 8
ID PA2A_HUMAN STANDARD; PRT; 144 AA.
AC P14555; Q9UCD2;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE (GTIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).
GN PLA2G2A OR PLA2B OR RASF-A OR PLA2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rheumatoid arthritic synovial fluid;
RX MEDLINE=89174566; PubMed=2925608;
RA Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
RA Kloss J., Johnson L.K.;
RT "Cloning and recombinant expression of phospholipase A2 present in
RT rheumatoid arthritic synovial fluid.";
RL J. Biol. Chem. 264:5335-5338(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174633; PubMed=2925633;
RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
RA Tizard R., Pepinsky R.B.;
RT "Structure and properties of a human non-pancreatic phospholipase
RT A2.";
RL J. Biol. Chem. 264:5768-5775(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91050834; PubMed=2239446;
RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
RT "Structure and properties of a secreted phospholipase A2 from human
RT platelets.";
RL Adv. Exp. Med. Biol. 275:35-53(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 21-144.
RC TISSUE=Spleen;
RX MEDLINE=89374261; PubMed=2775276;
RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
RT "The primary structure of a membrane-associated phospholipase A2 from
RT human spleen.";
RL Biochem. Biophys. Res. Commun. 163:42-48(1989).
RN [6]
RP SEQUENCE OF 21-54.
RC TISSUE=Synovial fluid;
RX MEDLINE=89197814; PubMed=3240982;
RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
RT "Amino acid composition and NH2-terminal amino acid sequence of human
RT phospholipase A2 purified from rheumatoid synovial fluid.";
RL J. Biochem. 104:326-328(1988).
RN [7]
RP SEQUENCE OF 21-33.
RC TISSUE=Synovial fluid;
RX MEDLINE=89076274; PubMed=3202859;
RA Lai C.Y., Wada K.;
RT "Phospholipase A2 from human synovial fluid: purification and
RT structural homology to the placental enzyme.";
RL Biochem. Biophys. Res. Commun. 157:488-493(1988).
RN [8]
RP SEQUENCE OF 21-75.
RC TISSUE=Ileal mucosa;
RX MEDLINE=94002200; PubMed=8399335;
RA Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
RT "Purification and characterization of a phospholipase A2 from human
RT ileal mucosa.";
RL Biochim. Biophys. Acta 1170:125-130(1993).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=91287826; PubMed=2062381;
RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
RA Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
RA Warrick M.W., Jones N.D.;
RT "Structure of recombinant human rheumatoid arthritic synovial fluid
RT phospholipase A2 at 2.2-A resolution.";
RL Nature 352:79-82(1991).

```


CC CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; U01119; AAC52936.1; -

DR HSP; P01458; IVP.

DR MGD; MGI:106638; Pla2g2c.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

KW Hydrolase; Lipid degradation; Calcium; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 150 GROUP IIC SECRETORY PHOSPHOLIPASE A2.

FT ACT_SITE 67 67 BY SIMILARITY.

FT ACT_SITE 115 115 BY SIMILARITY.

FT DISULFID 46 143 BY SIMILARITY.

FT DISULFID 48 64 BY SIMILARITY.

FT DISULFID 63 121 BY SIMILARITY.

FT DISULFID 69 150 BY SIMILARITY.

FT DISULFID 70 114 BY SIMILARITY.

FT DISULFID 79 107 BY SIMILARITY.

FT DISULFID 97 112 BY SIMILARITY.

FT DISULFID 99 105 POTENTIAL.

FT CARBOHYD 92 92 N-LINKED (GLCNAC...) (POTENTIAL).

FT CA_BIND 47 47 VIA CARBONYL OXYGEN (BY SIMILARITY).

FT CA_BIND 49 49 VIA CARBONYL OXYGEN (BY SIMILARITY).

FT CA_BIND 51 51 VIA CARBONYL OXYGEN (BY SIMILARITY).

FT CA_BIND 58 68 BY SIMILARITY.

FT CONFLICT 28 28 M -> W (IN REF. 2).

FT CONFLICT 77 77 Y -> W (IN REF. 2).

SO SEQUENCE 150 AA; 16983 MW; C2D5EF5E7B19972F CRC64;

Query Match 29.5%; Score 282; DB 1; Length 150;

Best Local Similarity 42.6%; Pred. No. 1.2e-18;

Matches 55; Conservative 15; Mismatches 49; Indels 10; Gaps 4;

QY 21 SLLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDWCMCHADCCYQELFDGCGH 80

Db 21 SFQFQRMVKKVHTGRSAFFSYGYCYGCGLGKGLPVDATDRCCWAHDCCVHKLKYECCQ 80

QY 81 PYVDYDHTIENNTETV-CSDLNKTECDKOTCMCDKNMVLCLMNO--TYREYRGFLNYY 137

Db 81 PILNAYQFTVNGTVTCGTVASSCPGQKACEDCKQSVCFKKNLATYKAFKQLF--- 137

QY 138 CGQPT-PNC 145

Db 138 ---PTRPQC 143

RESULT 14

PA2X_RAT STANDARD; PRT; 151 AA.

AC Q9QZT3;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Group X secretory phospholipase A2 precursor (EC 3.1.1.4)

DE (Phosphatidylcholine 2-acylhydrolase GX) (GX SPLA2) (sPLA2-X).

GN PLA2G10.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20002639; PubMed=10531313;

RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;

RT "On the diversity of secreted phospholipases A2. Cloning, tissue

RT distribution, and functional expression of two novel mouse group II

RT enzymes.";

RL J. Biol. Chem. 274:31195-31202(1999).

CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-

CC acyl groups in 3-sn-phosphoglycerides. Has a powerful potency for

CC releasing arachidonic acid from cell membrane phospholipids (By

CC similarity).

CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O -> 1-

CC acylglycerophosphocholine + a fatty acid anion.

CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; AF166100; AAF04501.1; -

DR HSP; P00593; 4BP2.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

KW Hydrolase; Lipid degradation; Calcium; Signal.

FT SIGNAL 1 17 BY SIMILARITY.

FT PROPEP 18 28 BY SIMILARITY.

FT CHAIN 29 151 GROUP X SECRETORY PHOSPHOLIPASE A2.

FT ACT_SITE 74 74 BY SIMILARITY.

FT ACT_SITE 119 119 BY SIMILARITY.

FT DISULFID 39 97 POTENTIAL.

FT DISULFID 53 143 BY SIMILARITY.

FT DISULFID 55 71 BY SIMILARITY.

FT DISULFID 70 125 BY SIMILARITY.

FT DISULFID 76 150 BY SIMILARITY.

FT DISULFID 77 118 BY SIMILARITY.

FT DISULFID 86 111 BY SIMILARITY.

FT DISULFID 104 116 BY SIMILARITY.

FT CA_BIND 54 54 VIA CARBONYL OXYGEN (BY SIMILARITY).

FT CA_BIND 56 56 VIA CARBONYL OXYGEN (BY SIMILARITY).

FT CA_BIND 58 58 VIA CARBONYL OXYGEN (BY SIMILARITY).

FT CA_BIND 75 75 BY SIMILARITY.

SO SEQUENCE 151 AA; 17088 MW; 2581E1520A455089 CRC64;

Query Match 29.5%; Score 282; DB 1; Length 151;

Best Local Similarity 36.7%; Pred. No. 1.3e-18;

Matches 54; Conservative 24; Mismatches 49; Indels 20; Gaps 5;

QY 12 GSVLSTA-----HGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDWCC 64

Db 12 GSVLSTA-----HGSLNLKAMVEAVTGRSAILSFVGYCYGCGLGGRGQPKDEVDWCC 64

QY 65 HAHDCYQELFDGCGHPPYVDHY-----DHTIENNTETVCSDLNKTECDKOTCMCDKNMVL 119

Db 65 HAHDCYQELFDGCGHPPYVDHY-----DHTIENNTETVCSDLNKTECDKOTCMCDKNMVL 119

QY 72 YHDCYQELFDGCGHPPYVDHY-----DHTIENNTETVCSDLNKTECDKOTCMCDKNMVL 151

Db 72 YHDCYQELFDGCGHPPYVDHY-----DHTIENNTETVCSDLNKTECDKOTCMCDKNMVL 151

QY 120 CLMNTQYREYRGFLNVCQPTPNC 146

Db 120 CLMNTQYREYRGFLNVCQPTPNC 146

QY 125 CLADTEVHLKYLFPFVLCCKDPSKCN 151

Db 125 CLADTEVHLKYLFPFVLCCKDPSKCN 151

RESULT 15

PA2A_MOUSE

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

P2A_MOUSE STANDARD; PRT; 146 AA.
P31482; Q60871;
01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
(phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
(GLIC SPUA2) (Enhancing factor) (EF).
PLA2G2A.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=BALB/c;
Mulherkar R.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Intestine;
MEDLINE=95403435; PubMed=7673223;
Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
Ywan M., Tang C., Rancourt D.E., Cromlish W.;
"A natural disruption of the secretory group II phospholipase A2 gene
in inbred mouse strains.";
J. Biol. Chem. 270:22378-22385(1995).
[3]
SEQUENCE OF 22-146 FROM N.A.
STRAIN=BALB/c; TISSUE=Small intestine;
MEDLINE=94029955; PubMed=8267767;
Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
"Enhancing factor, a Paneth cell specific protein from mouse small
intestines; predicted amino acid sequence from RT-PCR amplified cDNA
and its expression";
Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
[4]
ERRATUM.
MEDLINE=94071967; PubMed=8250944;
Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
Biochem. Biophys. Res. Commun. 197:351-352(1993).
[5]
SEQUENCE OF 29-146 FROM N.A.
STRAIN=C3H;
Macphree M., Chepenik K.P., Liddell R.A., Nelson K.K.,
Siracusa L.D., Buchberg A.M.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
[6]
PRELIMINARY SEQUENCE OF 22-41.
TISSUE=Small intestine;
MEDLINE=93146172; PubMed=8425615;
Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;
"Enhancing factor protein from mouse small intestines belongs to the
phospholipase A2 family.";
FEBS Lett. 317:263-266(1993).
-1- FUNCTION: MAY PLAY A ROLE IN CELL PROLIFERATION, BY INCREASING THE
BINDING OF EGF TO THE CELLS AND THEREBY MODULATING ITS ACTION. IN
DOING SO, THIS ISOZYME BINDS TO A MEMBRANE-ASSOCIATED RECEPTOR
DISTINCT FROM THE EGF RECEPTOR AND WHICH COULD BE A HEPARAN-
SULFATE PROTEOGLYCAN LOCATED ON THE CELL MEMBRANE.
-1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2'-ACYL GROUPS IN 3-SN-PHOSPHOLIPIDES.
-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
-1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-1- SUBCELLULAR LOCATION: Membrane-associated.
-1- TISSUE SPECIFICITY: MAINLY IN THE PANETH CELLS ADJACENT TO THE
STEM POPULATION IN THE SMALL INTESTINES. ALSO EXPRESSED IN
REGENERATING LIVER AND HYPERPLASTIC OESOPHAGEAL EPITHELIUM.
-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -

Search completed: February 10, 2003, 10:35:49
Job time : 13 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:28 ; Search time 31 Seconds
(without alignments)
1116.642 Million cell updates/sec

Title: US-09-975-456B-2

Perfect score: 957

Sequence: 1 MKKFTVAILAGSVLSTAHG.....EPPPEVTCTSHQSPAPPAPP 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	42.0	69	Q9H415	Q9H415 homo sapien
2	319.5	33.4	138	Q90777	Q90777 trimeresuru
3	295.5	30.9	137	Q8UW08	Q8UW08 bothriechis
4	294.5	30.8	122	Q42187	Q42187 agkistrodon
5	290.5	30.4	138	Q91968	Q91968 trimeresuru
6	290	30.3	154	Q90X68	Q90X68 mesocricetu
7	287.5	30.0	146	Q91Y34	Q91Y34 rattus norv
8	284.5	29.7	122	Q42188	Q42188 agkistrodon
9	280.5	29.3	138	Q90W39	Q90W39 trimeresuru
10	277.5	29.0	138	Q90Z29	Q90Z29 echis color
11	269	28.1	138	Q92147	Q92147 trimeresuru
12	267.5	28.0	138	Q90395	Q90395 crotalus sc
13	263.5	27.5	138	Q8UV26	Q8UV26 crotalus at
14	263	27.5	122	Q42192	Q42192 agkistrodon
15	262.5	27.4	137	Q8UV27	Q8UV27 crotalus at
16	261.5	27.3	137	Q8UVU7	Q8UVU7 cerrophidio

17	258.5	27.0	137	13	Q92152	Q92152 trimeresuru
18	258	27.0	138	13	Q9PVF3	Q9PVF3 agkistrodon
19	251.5	26.3	122	13	Q91521	Q91521 vipera ammo
20	250.5	26.2	124	13	Q42190	Q42190 agkistrodon
21	249	26.0	137	13	Q91967	Q91967 vipera ammo
22	249	26.0	138	13	Q92118	Q92118 trimeresuru
23	247.5	25.9	119	13	Q91AT9	Q91AT9 bochrops ne
24	245	25.6	124	13	Q42189	Q42189 agkistrodon
25	243.5	25.4	138	13	Q9PWR6	Q9PWR6 vipera pala
26	243.5	25.4	138	13	Q8UV25	Q8UV25 agkistrodon
27	242.5	25.3	138	13	Q57385	Q57385 agkistrodon
28	242.5	25.3	138	13	Q80C87	Q80C87 bochrops in
29	241.5	25.2	137	13	Q9PVF4	Q9PVF4 agkistrodon
30	240	25.1	139	13	Q9PVF2	Q9PVF2 trimeresuru
31	235	24.6	122	13	Q91506	Q91506 echis color
32	233.5	24.4	138	13	Q910A0	Q910A0 vipera ammo
33	232.5	24.3	138	13	Q910A1	Q910A1 vipera ammo
34	232	24.2	139	13	Q9PVE9	Q9PVE9 agkistrodon
35	228.5	23.9	122	13	Q918F8	Q918F8 bothrops pl
36	227.5	23.8	139	13	Q92151	Q92151 trimeresuru
37	224	23.4	137	13	P79836	P79836 trimeresuru
38	221	23.1	126	13	Q9PVF1	Q9PVF1 agkistrodon
39	220	23.0	137	13	Q9YGJ7	Q9YGJ7 vipera pala
40	218	22.8	126	13	Q9PVF0	Q9PVF0 agkistrodon
41	218	22.8	149	13	Q9YH62	Q9YH62 dicentrarch
42	210	21.9	145	13	Q9DF52	Q9DF52 bungarus ca
43	210	21.9	152	13	Q8UW31	Q8UW31 lapemis har
44	206.5	21.6	145	13	Q9QW48	Q9QW48 bungarus fa
45	206.5	21.6	145	13	Q9QW47	Q9QW47 bungarus fa

ALIGNMENTS

RESULT 1

Q9H415 ID Q9H415 PRELIMINARY; PRT; 69 AA.
AC Q9H415;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DJ340N1.1 (Novel phospholipase similar to mouse phospholipase A2 group
DE IIF (PLA2G2F) (Fragment)).
GN DJ340N1.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z98257; CAC12707.1; -;
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
FT NON_TER 1
SQ SEQUENCE 69 AA; 7828 MW; D8CA44FC93040ED7 CRC64;

Query Match 42.0%; Score 402; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 DLNKTCEKQTCMKCDKNVLCMNQTYREYRGFLNVYCGPTPNCISYEPPPEVTCTSH 159
Db 1 DLNKTCEKQTCMKCDKNVLCMNQTYREYRGFLNVYCGPTPNCISYEPPPEVTCTSH 60

QY 160 QSPAPPAPP 168

Db 61 QSPAPPAPP 69

RESULT 2

Q90Y77 PRELIMINARY; PRT; 138 AA.

ID Q90Y77

AC 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Phospholipase A2 isoenzyme PL-Y.

GN

OS Trimeresurus flavoviridis (Habu).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Trimeresurus.

OX NCBI_TaxID=88087;

RN [1]

RN SEQUENCE FROM N.A.

RP Chijawa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,

RA Nakashima K., Oda-Ueda N., Shimohigashi Y., Fukumaki Y., Hattori S.,

RA Ohno M.;

RT "Regional evolution of Trimeresurus flavoviridis venom-gland

RT phospholipase A2 isozymes.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

RL EMBL; AB072173; BAB68546.1; -

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF000068; phoslip; 1.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR PROSITE; PS00119; PA2_ASP; UNKNOWN.1.

DR PROSITE; PS00118; PA2_HIS; UNKNOWN.1.

SQ SEQUENCE 138 AA; 15729 MW; C96B1E878C8A1196 CRC64;

Query Match 33.4%; Score 319.5; DB 13; Length 138;

Best Local Similarity 40.1%; Pred. No. 1.7e-27;

Matches 59; Conservative 28; Mismatches 49; Indels 11; Gaps 5;

QY 1 MKKFFTVAILAGSVLSTAGHSLNKKAMVEAVTGRSAILSFFVGYCGYGLGGRGQPKDEV 60

Db 1 MRTLWIMAVL---LVGVEGHLLOFRMKIKMTGKEPIVSFAFYGYCGYGGGRGPKDAT 56

QY 61 DWCHAHDCCYQELFDQCHPYVDHYDHTIENNTIEVCSDLNKTCDKQFCMCDKNVLC 120

Db 57 DRCCFVHDCCEYK---TGCNPLTDYSHSLNKT-IVGGE-NK-PCLKEMCECDKAAIAC 111

QY 121 LMN--QTYREYRGFLNYVCOGPTNC 145

Db 112 FRDLNLTYYKKRYMTFPDICTDPTKEC 138

RESULT 3

Q8UVU8 PRELIMINARY; PRT; 137 AA.

AC Q8UVU8

DT 01-MAR-2002 (TREMELrel. 20, Created)

DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Lys-49 phospholipase A2-like protein.

OS Bothriechis schlegelii (Eyelash palm pitviper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothriechis.

OX NCBI_TaxID=44725;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=2147853; PubMed=11594738;

RA Tsai I.H., Chen Y.H., Wang Y.M., Tu M.C., Tu A.T.;

RT "Purification, Sequencing, and Phylogenetic Analyses of Novel Lys-49

RT Phospholipases A(2) from the Venoms of Rattlesnakes and other Pit

RT Vipers.";

RL Arch. Biochem. Biophys. 394:236-244(2001).

DR EMBL; AF374236; AAL39065.1; -

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF000068; phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; UNKNOWN.1.

DR PROSITE; PS00118; PA2_HIS; UNKNOWN.1.

SQ SEQUENCE 137 AA; 15285 MW; OD588DEIAC84D00D CRC64;

Query Match 30.9%; Score 295.5; DB 13; Length 137;

Best Local Similarity 40.6%; Pred. No. 7.5e-25;

Matches 58; Conservative 27; Mismatches 47; Indels 11; Gaps 6;

QY 1 MKKFFTVAILAGSVLSTAGHSLNKKAMVEAVTGRSAILSFFVGYCGYGLGGRGQPKDEV 60

Db 1 MRTLWIMAVL---LVGVEGSMIEGKMLLETGKNAATSYIAYGCGYGGRRGQPLDAT 56

QY 61 DWCHAHDCCYQELFDQCHPYVDHYDHTIENNTIEVCSDLNKTCDKQTCMCDKNVLC 120

Db 57 DRCCYVHKCCYKKL--TGCNPLTDYSHSLNKT-IVGGE-NK-PCLKEMCECDKAAIAC 111

QY 121 LMN--QTYREYRGFLNYVCOGP 141

Db 112 LGKNVNTYNNKYKITMKMECKRP 134

RESULT 4

O42187 PRELIMINARY; PRT; 122 AA.

ID O42187

AC O42187

DT 01-JAN-1998 (TREMELrel. 05, Created)

DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Phospholipase A2 (Fragment).

OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys

OS pallas).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Gloydius.

OX NCBI_TaxID=8714;

RN [1]

RN SEQUENCE FROM N.A.

RP Pan H., Wu X.F., Ouyang L.L., Liu X.L., Yang G.Z.;

RT "cDNA of phospholipase A2 from Agkistrodon halys Pallas.";

RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF015242; AAB71844.1; -

DR HSSP; P51972; 1VAP.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF000068; phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

FT NON_TER 1

SQ SEQUENCE 122 AA; 13892 MW; 4980CGAA5E648EAE CRC64;

Query Match 30.8%; Score 294.5; DB 13; Length 122;

Best Local Similarity 40.9%; Pred. No. 8.5e-25;

Matches 52; Conservative 23; Mismatches 45; Indels 7; Gaps 4;

QY 21 SILNLKAMVEAVTGRSAILSFFVGYCGYGLGGRGQPKDEVDMCHAHDCCYQELFDQCH 80

Db 1 SLLOFRKMIKKMTGKEPVVSYAFYGYCGYGGGRGPKDATDRCCFVHDCCEYK--TGCD 58

QY 81 PVVDHYDHTIENNTIEVCSDLNKTCDKQTCMCDKNVLCMLN--QTYREYRGFLNYV 138

Db 59 PKWDDYTSWKNGT-IVCG--GDDPCKEVCECDKAAIACFDNLKTYKKRYMYPNLC 115

QY 139 QGPTPNC 145

Db 116 SSKSEK 122

RESULT 5

Q91968 PRELIMINARY; PRT; 138 AA.

ID Q91968

AC Q91968;

DR	SWART; SW00085; PA2c;	1.
DR	PROSITE; PS00119; PA2_ASP; UNKNOWN_1.	
DR	PROSITE; PS00118; PA2_HIS; UNKNOWN_1.	
KW	Hydrolase; Signal.	
FT	SIGNAL	1 21 POTENTIAL
FT	CHAIN	22 15A SRC-ASSOCIATED PHOSPHOLIPASE A2.
SO	SEQUENCE	154 AA; 17217 MW; F5E0A76CE441772C CRC64;
 Query Match Best Local Similarity 30.3%; Score 290; DB 11; Length 154; Matches 57; Conservative 17; Mismatches 51; Indels 4; Gaps		
QY	20 GSLLNLKAMVEAVTGRSAILSFVGYGCGLGGRGQPDKDEVMCCAHADCCYQLPDQC	79
Dd	: :	
Dd	21 GSLAEINRMIIQTGTMRAGLSYAFYGCHGLGSGRPKDATDWCCAHDCCYDRLDLGC	80
QY	80 HPYVDHYDHTEIENNTETVCSDLANKTCDKOTCMCKDNMVLCLM--NQTYREERYRGLFNLY	137
Dd	: : : : : : : :	:
Dd	81 GTKSLDYNFKYSRG-EITCS-VNQDFCGOOLCHDRLLAEQAQHOKSYSKMYLMGIKKS	138
QY	138 COGPTPNCS	146
Dd	: :	:
Dd	139 CEGESPSCS	147
 RESULT 7		
Q91V34	PRELIMINARY;	PRT; 146 AA.
ID	Q91V34	
AC	Q91V34;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DRC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DS	Platelet phospholipase A2 precursor (Fragment).	
OE	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;	
NCBI_TaxID=10116;	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=WISTAR; TISSUE=BLOOD;	
RA	Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;	
RT	"Cloning and sequence determination of rat platelet phospholipase A2 from whole blood.";	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL: AF3635363; AAK52061.1; "	
DR	InterPro: IPR001211; PhospholipaseA2.	
DR	Fam; PF00068; Phoslip; 1.	
DR	ProDom; PD000303; PhospholipaseA2; 1.	
DR	PROSITE; PS00119; PA2_ASP; UNKNOWN_1.	
DR	PROSITE; PS00118; PA2_HIS; UNKNOWN_1.	
KW	Signal.	1 21 POTENTIAL
FT	SIGNAL	22 >146 PLATELET PHOSPHOLIPASE A2.
FT	NON_TER	146 146
SO	SEQUENCE	146 AA; 16306 MW; 60C1C9EC85DCBD67 CRC64;
 Query Match Best Local Similarity 41.5%; Score 287.5; DB 11; Length 146; Matches 59; Conservative 19; Mismatches 57; Indels 7; Gaps		
QY	7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGSRATSLFVGVCYLGGRGQPKDEVDMWCCH	65
Dd	: : :	: : : :
Dd	9 VVIWAFGSI--QVOGSLLEFGQMIPKTKRADVSIVGFVGHGVGCRGSPKDATTMCVV	66
QY	66 AHGCCYQLFDQGCVHYPVDHYDHTIEINTETVCSDLNKTECDKQTCMDCKNMVLCLM--N	123
Dd	:	: : :
Dd	67 THDCCYNLRLEKRCGKGKELTYKFYSIRG-RISCSTNQDSCRKLQCCDKAAACEFAARN	124
QY	124 QTYREERYRGLFNLYCOGPTPNC	145
Dd	: : : : :	:
Dd	125 KYSLSKYQFYPPNFKECFKGTTPSC	146

DE acylhydrolase (Lecithinase A) (PHOSPHATIDASE) (PHOSPHATIDOLIPASE).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Ogawa T.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93317604; PubMed=8327468;
RA Nakashima K., Ogawa T., Oda N., Hattori M., Sakaki Y., Kihara H.,
RA Ohno M.;
RT "Accelerated evolution of Trimeresurus flavoviridis venom gland
phospholipase A2 isozymes.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5964-5968(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=94369106; PubMed=7765285;
RA Nakashima K., Nobuhisa I., Ogawa T., Hattori M., Sakaki Y., Kihara H.,
RA Ohno M.;
RT "Polymorphisms of Trimeresurus flavoviridis venom gland phospholipase
A2 isozyme genes.";
RL Biosci. Biotechnol. Biochem. 58:1510-1511(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=95296360; PubMed=7777556;
RA Nakashima K., Nobuhisa I., Deshimaru M., Nakai M., Ogawa T.,
RA Shimohigashi Y., Fukumaki Y., Hattori M., Sakaki Y., Hattori S.,
RA Ohno M.;
RT "Accelerated evolution in the protein-coding regions is universal in
crotalinae snake venom gland phospholipase A2 isozyme genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:5605-5609(1995).
CC -/- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-
CC -/- COFACTOR: CALCIUM.
CC ACYLGLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
DR EMBL; D10725; BAA01568.1; -;
DR EMBL; D10723; BAA01566.1; -;
DR HSSP; P14418; 1BK9.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR PRODOM; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL. 1 16 POTENTIAL.
FT CHAIN 17 138 PHOSPHOLIPASE A2.
SQ SEQUENCE 138 AA; 15708 MW; AAD7DC04A6EDA975 CRC64;
Query Match 28.1%; Score 269; DB 13; Length 138;
Best Local Similarity 37.7%; Pred. No. 6.5e-22;
Matches 57; Conservative 21; Mismatches 59; Indels 14; Gaps 5;
QY 1 MKKFTTVAIIAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGGLGRGPKDEV 60
Db 1 MRTLWIMAVL-----LVGVGHLQMFENMKKVTGRSGIWMWYSGYCYGKGGRFPDPS 56
QY 61 DMCCHAHDCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCKDNMVL 120
Db 57 DRCCFVHDCCYGVK--TGCDPKDDFYIYSSENG-DIVCGD--DDLCKKEVCECDKAAIC 111
QY 121 LMNQTREEYRGFLNVCYCGPTNCPNC 151
Db 112 -----FRDNMDTYQNKYWFYPASCKESEP 137

RESULT 12
Q90395 PRELIMINARY; PRT; 138 AA.
ID Q90395;
AC Q90395;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Preproacidic subunit of mojave toxin precursor.
OS Crotalus scutulatus scutulatus (Mojave rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8738;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=94156205; PubMed=8112610;
RA John T.R., Smith L.A., Kaiser I.I.;
RT "Genomic sequences encoding the acidic and basic subunits of Mojave
toxin; unusually high sequence identity of non-coding regions.";
RL Gene 139:229-234(1994).
DR EMBL; U01026; AAC59673.1; -;
DR HSSP; P00624; 1PP2.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR PRODOM; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL. 1 16 POTENTIAL.
FT CHAIN 17 138 PROACIDIC SUBUNIT OF MOJAVE TOXIN.
SQ SEQUENCE 138 AA; 15211 MW; 8164C7C8D27D6EBE CRC64;
Query Match 28.0%; Score 267.5; DB 13; Length 138;
Best Local Similarity 38.8%; Pred. No. 9.6e-22;
Matches 57; Conservative 18; Mismatches 61; Indels 11; Gaps 5;
QY 1 MKKFTTVAIIAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYCYGGLGRGPKDEV 60
Db 1 MRALWIVAVL----LVGVGSLVEFETLMKTAGRSIGSYSSYCYGCGAGQGWPDAS 56
QY 61 DMCCHAHDCCYQELFDGCHPYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCKDNMVL 120
Db 57 DRCCFVHDCCYAKL--TGCDPTDVTYRQEDG-EIVCG--GDDPCGTQICECDRAAIC 111
QY 121 LMN--QTYREEYRGFLNVCYCGPTNCPNC 145
Db 112 FRDSMNTYDYKYLRFSPENCQGESQPC 138
RESULT 13
Q8UVZ6 PRELIMINARY; PRT; 138 AA.
ID Q8UVZ6;
AC Q8UVZ6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acidic phospholipase A2 precursor.
OS Crotalus atrox (Western diamondback rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8730;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.;
RT "Cloning, characterization and phylogeny of two novel Lys-49
phospholipase A2 from Crotalus atrox and Deinagkistrodon acutus venom
glands.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF269131; AAL36974.1; -;
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
DR PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 138 ACIDIC PHOSPHOLIPASE A2.
SQ SEQUENCE 138 AA; 15346 MW; 78A0034CA96344E3 CRC64;

Query Match 27.5%; Score 263.5; DB 13; Length 138;
Best Local Similarity 36.8%; Pred. No. 2.7e-21;
Matches 56; Conservative 20; Mismatches 61; Indels 15; Gaps 6;

QY 1 MKKFTTVAIIAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYGCGGLGRGQPKDEV 60
Db 1 MRTLWIIVAVL-----LLGVEGSLVQFETLIMKIAGRGLLWYSAYGCGYCGWGHGLPQDAT 56

QY 61 DMCCHADCCYQELFDGCHPYVDHYDHTIENNTIEVCSDLNTECDKQTCMCKNNVLC 120
Db 57 DRCCFVHDCYGRATD--CPKIVSTYIS--EENGELICG--GDDPGCTQICECDKAAIIC 111

QY 121 LMNQTYREYRGFLNVYCGQTPNCSIYEPP 152
Db 112 ----FRDNPSPYDNKYWLPFPKNCR--EEPEP 137

RESULT 14

O42192 ID 042192 PRELIMINARY; PRT; 122 AA.
AC O42192;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A2 (Fragment).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RA Pan H., Wu X.F., Ouyang L.L., Liu X.L., Yang G.Z.;
RT "cDNA of phospholipase A2 from Agkistrodon halys Pallas.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF015247; AAB71849.1; -;
DR HSSP; P14418; 1BK9.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
FT NON_TER 1
SQ SEQUENCE 122 AA; 13666 MW; C7D21D90CBE1F314 CRC64;

Query Match 27.5%; Score 263; DB 13; Length 122;
Best Local Similarity 39.7%; Pred. No. 2.6e-21;
Matches 52; Conservative 18; Mismatches 51; Indels 10; Gaps 4;

QY 21 SLNLLKAMVEAVTGRSAILSFVGYGCGGLGRGQPKDEVDMCCHADCCYQELFDGCH 80
Db 1 SLMQFTLIMKIAGRGLLWYSAYGCGYCGWGHGLPQDATSCCFVHDCYGRK--TGCN 58

QY 81 PYVDHYDHTIENNTIEVCSDLNTECDKQTCMCKNNVLC LMNQTYREYRGFLNVYCGQ 140
Db 59 PKMDVITYT--EENGAVICG--GDDPCKKQICECDKDAIC-----FRDNIIDYDNKYWFF 110

QY 141 PTPNCISIYEPP 151
Db 111 PAKNCQESEP 121

RESULT 15

Q8UVZ7 ID Q8UVZ7 PRELIMINARY; PRT; 137 AA.
AC Q8UVZ7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Lys-49 phospholipase A2 precursor.
OS Crotalus atrox (Western diamondback rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8730;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.;
RT "Cloning, characterization and phylogeny of two novel Lys-49 phospholipase A2 from Crotalus atrox and Deinagkistrodon acutus venom glands.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF269130; AAL36973.1; -;
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
DR PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 137 LYS-49 PHOSPHOLIPASE A2.
SQ SEQUENCE 137 AA; 15597 MW; 63E5F80D0565AEE6 CRC64;

Query Match 27.4%; Score 262.5; DB 13; Length 137;
Best Local Similarity 39.2%; Pred. No. 3.4e-21;
Matches 56; Conservative 27; Mismatches 49; Indels 11; Gaps 6;

QY 1 MKKFTTVAIIAGSVLSTAHGSLNLLKAMVEAVTGRSAILSFVGYGCGGLGRGQPKDEV 60
Db 1 MRTFWIVAML-----LVGVEGSLVGLKMILOETGKNPITSYGIYGCNGCGVSRHKPKDGT 56

QY 61 DMCCHADCCYQELFDGCHPYVDHYDHTIENNTIEVCSDLNTECDKQTCMCKNNVLC 120
Db 57 DECCFVHCKCYKKLTD--CDPKMDGYTYSFKDKT--IIC-DVN-NPCLKEMCECDKAVAIC 111

QY 121 LMN--QTYREYRGFLNVYCGQ 141
Db 112 LRENLDYTKKYIYPKFLCKKP 134

Search completed: February 10, 2003, 10:37:09
Job time : 32 secs